

**O'Bryen, Barbara**

---

**From:** Switzer, Juliet  
**Sent:** Thursday, December 18, 2003 8:37 AM  
**To:** O'Bryen, Barbara  
**Subject:** please search

09/889491

please search seq id no 13 and 14 in all prior art databases. please also search in reg file in oligos of 100 or fewer crossed as appropriate with alignments. Thanks.

Juliet Switzer  
Art Unit 1634  
703 306 5824  
office CM1 12D15  
mailbox CM1 12E12













NGUYEN, C., NICOL, R., NOTHU, C., O'CONNOR, F., O'DONNELL, P.,  
 KELL, D., OLIVER, J., PETERSON, K., PUNNINGHAM, P., RABIER, B.,  
 ROMAN, J., SCHUUR, R., SCHUBACK, R., SEANAY, S., SEANAY, P.,  
 SPENCER, J., STANGE, S., THODOU, N., STOJANOVIC, N., STUBBS, M.,  
 TALAMAS, J., TAYLOR, S., THODOU, J., TOPP, K., TRAVIS, M.,  
 WYMAN, D., YOUNG, G., ZATOUN, J., ZEBEK, J., ZIMMER, A. and ZODY, M.,  
 Direct Submission  
 Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 200 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smt. A. P.N. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIRS  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submission@genome.wi.mit.edu  
 Center project name: 12561

----- Summary Statistics -----  
 Sequencing vector: plasmid, 100% of reads  
 Chemistry: Dye-terminator: Big Dye3, 100% of reads  
 Assembly program: Phrap; version 0.960701  
 Consensus quality: 154720 bases at least Q40  
 Consensus quality: 154877 bases at least Q40  
 Consensus quality: 154939 bases at least Q20  
 Insert size: 150000; agarose-fp  
 Insert size: 154929; sum-of-contigs  
 Quality coverage: 11.5 in Q20 bases; sum-of-contigs  
 Quality coverage: 11.5 in Q40 bases; sum-of-contigs  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. Gaps between the contigs  
 \* are represented by dashes. The sequence is  
 \* believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* been provided by the submitter.  
 \* This sequence will be replaced  
 \* by a higher quality version as it is available and  
 \* the accession number will be preserved.  
 \* -----  
 1 30191: contig of 30191 bp in length  
 30192 30291: gap of 100 bp  
 30193 30292: gap of 100 bp  
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 30667













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repeat_region      comp.fam1="AluX"      /ipc.fam1="AluX"
                    complement(3605,.36850)
                    /ipc.fam1="AluX"
repeat_region      complement(3685,.37044)
                    /ipc.fam1="AluP45"
repeat_region      37192..37233NR rich"
                    complement(37233..37233)
repeat_region      38354..38654AluSp"
                    /ipc.fam1="AluP12"
                    complement(37278..37715)
repeat_region      38676..38683AluSp"
                    /ipc.fam1="AluP13"
                    complement(39541..39697)
repeat_region      39541..39697
                    /ipc.fam1="AluP"
                    complement(4107..4107)
repeat_region      41163..41480
                    /ipc.fam1="(TA)n"
repeat_region      41163..41480
                    /ipc.fam1="MER2"
                    complement(41483..41521)
repeat_region      42047..42086
                    /ipc.fam1="(CA)n"
                    complement(42047..42086)
repeat_region      /ipc.fam1="(TA)n"

```

```

Query MARCH
Best Local Similarity 74.2%; Score 23; DB 9; Length 20223;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Job time : 139c 89 secs

```

```

07 1 ATGCTGAAAAGTCTGTAATTCGAAATTTT 31
    |||||
DB 109532 ATTTGAGACCTTAAAGTATTTTAAATTTT 109502

```

=> fil reg; d que 13

FILE 'REGISTRY' ENTERED AT 09:22:13 ON 18 DEC 2003  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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Property values tagged with IC are from the ZIC/VINITI data file  
provided by InfoChem.

STRUCTURE FILE UPDATES: 17 DEC 2003 HIGHEST RN 627482-61-5  
DICTIONARY FILE UPDATES: 17 DEC 2003 HIGHEST RN 627482-61-5

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2003

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more  
information enter HELP PROP at an arrow prompt in the file or refer  
to the file summary sheet on the web at:  
<http://www.cas.org/ONLINE/DBSS/registryss.html>

L2 9 SEA FILE=REGISTRY ABB=ON AUAUAGAAGCCCAAGAAAAAUCAGCUGACC|GGUCAG  
CUGAUUUUUUCUUGGGCUUCUAU|AUAGUGAAAAACUGUGUAAUUAUGAAAAUUU|AAAAUU  
UCAUAAUUACACAAGUUUUCACU|SQSN  
L3 4 SEA FILE=REGISTRY ABB=ON L2 AND SQL<101

*Aug 13.3-14*  
*S. Thier*  
*Supplements*

=> d rn cn kwic nte lc 1-4

L3 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 290212-93-0 REGISTRY  
CN GenBank AX028511 (9CI) (CA INDEX NAME)  
SQL 31

SEQ 1 atagtgaaaa cttgtgtaat tatgaaattt t  
=====

HITS AT: 1-31

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

LC STN Files: GENBANK

L3 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 290212-92-9 REGISTRY  
CN GenBank AX028510 (9CI) (CA INDEX NAME)  
SQL 30

SEQ 1 atatagaagc ccaagaaaaa tcagctgacc  
=====

HITS AT: 1-30

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

LC STN Files: GENBANK

L3 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 286027-93-8 REGISTRY  
CN 14: PN: WO0042216 SEQID: 14 unclaimed DNA (9CI) (CA INDEX NAME)  
SQL 31

SEQ 1 atagtgaaaa cttgtgtaat tatgaaattt t

HITS AT: 1-31

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

LC STN Files: CA, CAPLUS

L3 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN  
RN 286027-92-7 REGISTRY  
CN 13: PN: W00042216 SEQID: 13 unclaimed DNA (9CI) (CA INDEX NAME)  
SQL 30

SEQ 1 atatagaagc ccaagaaaaa tcagctgacc

HITS AT: 1-30

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

LC STN Files: CA, CAPLUS

=> fil capl; s 13

FILE 'CAPLUS' ENTERED AT 09:22:48 ON 18 DEC 2003  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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FILE LAST UPDATED: 17 Dec 2003 (20031217/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2000:493707 CAPLUS  
DOCUMENT NUMBER: 133:130737  
TITLE: Genetic predisposition to abnormal calcification condition such as osteoporosis  
INVENTOR(S): Kusk, Philip  
PATENT ASSIGNEE(S): Osteometer Biotech A/S, Den.  
SOURCE: PCT Int. Appl., 70 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.

KIND DATE

APPLICATION NO. DATE



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WO 2000042216      A2      20000720      WO 2000-EP319      20000117  
WO 2000042216      A3      20001102  
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,  
CZ, DE, DK, DM, EE, ES, FI, GE, GD, GE, GH, GM, HR, HU, ID, IL,  
IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,  
MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,  
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,  
AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,  
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,  
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG  
EP 1144686      A2      20011017      EP 2000-909076      20000117  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,  
IE, SI, LT, LV, FI, RO

## PRIORITY APPLN. INFO.:

GB 1999-1037      A 19990118  
GB 1999-12585      A 19990528  
WO 2000-EP319      W 20000117

- AB Methods of assessing an individual's predisposition to abnormal  
calcification conditions such as osteoporosis by detg. the genotype of a  
promoter for the bone sialoprotein gene, the matrix gla protein gene, the  
osteopontin gene or the osteoprotegerin gene individually or in any  
combination. Specific allelic variations for each promoter are described.
- IT 286027-92-7 286027-93-8  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; genetic predisposition to abnormal  
calcification condition such as osteoporosis)

FILE 'HOME' ENTERED AT 09:22:55 ON 18 DEC 2003





XX Olek A, Pispembrock C, Berlin K,  
DB WPI: 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
XX cytosine methylation

XX Claim 1, SEQ ID NO 1945; 32bp + Sequence Listing, German.

XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/aliceptive bowel  
CC diseases. The present sequence is a gene of the invention.

XX Sequence 7771 BP; 2788 A; 45 C; 1303 G; 3635 T; 0 other;

XX Query March 89.7%; Score 37.8; DB 24; Length 7771;  
XX Best Local Similarity 93.5%; Pred.No.1.1;  
XX Matches 25/ Conservative 0/ Mismatches 2/ Indels 0/ Gaps 0/

XX 1 ATGTGTAACCTGTGTGATTTGAAATTTT 31

XX DB 4650 ATGTGTAACCTGTGTGATTTGAAATTTT 4680

XX RESULT 4  
XX HJL3373/73  
XX HJL3373/73 standard; DNA; 7771 BP.

XX ABL33973;

XX 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 1946.

XX Human immune system disease; cytosine methylation; antineoplastic;  
XX antitumor; antitumor; antineoplastic; antineoplastic; neoplastic;  
XX neuroprotective; anti-IV; anticonvulsant; ophthalmological;  
XX antineoplastic; antitumor; antineoplastic; antineoplastic;  
XX antineoplastic; cancer; eye disease; antineoplastic; anemia;  
XX antineoplastic; cancer; eye disease; antineoplastic; anemia;  
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
XX gene; da.

XX Homo sapiens.

XX W0200200928-A2.

XX 03-JAN-2002.

XX 02-JUL-2001, 2001WO-EP07537.

XX 30-JUN-2000, 2000DE-102229.

XX 01-SEP-2000, 2000DE-103625.

XX (EPIC) - EPICENTRICS AG.

XX Olek A, Pispembrock C, Berlin K,

XX WPI: 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
XX cytosine methylation

XX Claim 1, SEQ ID NO 1946; 32bp + Sequence Listing, German.

CC The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/aliceptive bowel  
CC diseases. The present sequence is a gene of the invention.

XX Sequence 7771 BP; 2145 A; 45 C; 1537 G; 4046 T; 0 other;

XX Query March 74.2%; Score 23; DB 24; Length 7771;  
XX Best Local Similarity 83.5%; Pred.No. 50;  
XX Matches 26/ Conservative 0/ Mismatches 5/ Indels 0/ Gaps 0/

XX 1 ATGTGTAACCTGTGTGATTTGAAATTTT 31

XX DB 3122 ATGTGTAACCTGTGTGATTTGAAATTTT 3092

XX RESULT 5  
XX ABL26253  
XX ABL26253 standard; cDNA; 134 BP.

XX ABL26253;

XX 11-FEB-2003 (first entry)

XX Human GDP-mannose 4,6-dehydrogenase (GM4,6D) DNA #8310.

XX Human; GDP-mannose 4,6-dehydrogenase; GM4,6D; gene; sis; inflammation;  
XX cellular; fructose; glycosyltransferase; fructose; fructose; fructose;  
XX complex carbohydrate; gene replacement therapy; immunosuppressive;  
XX anti-inflammatory; antitumor; antibacterial; cerebroprotective;  
XX antineoplastic; vasotropic.

XX Homo sapiens.

XX US200210548-A1.

XX 15-AUG-2002.

XX 11-JUN-2001, 2001US-0879574.

XX 23-NOV-1996, 96US-075323.

XX 03-DEC-1997, 97US-0984246.

XX 09-FEB-1998, 98US-0149674.

XX 14-JUN-1999, 99US-0331177.

XX (GENV) GENETICS INST INC.

XX Sullivan P, Kitz R, Kumar R;

XX WPI: 2003-066573/06.

XX New composition comprising GDP-mannose 4,6-dehydrogenase (GM4,6D)  
PT peptide, for manufacturing complex carbohydrate, or as targets for  
XX screening GM4,6D antagonists for treating e.g. arthritis, or transplant  
XX rejection

XX Disclosure; SEQ ID NO 8313; 69p; English.

XX The invention relates to a composition comprising a human GDP-mannose  
CC 4,6-dehydrogenase (GM4,6D) peptide. The peptide is useful for identifying  
CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation  
CC in a mammalian subject and for treating or ameliorating diseases affected  
CC by inflammation and/or autoimmunity. These diseases include arthritis,  
CC rheumatoid arthritis, asthma, psoriasis, repetitive injury, stroke or  
CC infection. The GM4,6D peptide or a polynucleotide encoding it is also  
CC useful for identifying and screening for antagonists of the activity of the enzyme. The  
CC screening small molecule antagonists of the activity of the enzyme. The

CC polynucleotide is useful in developing an assay for defects in the  
 CC sequence, as in the case of the present invention. Sequences encoding  
 CC human GM4, 6D peptides of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html.

SO Sequence 134 BP, 40 A, 13 C, 25 G, 56 T, 0 other;

Query Match

Best Local Similarity 72.9%; Score 22.6; DB 25; Length 134;

Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 2 1ATGGAAGAACTGTGATATTCGATTAATTT 30

33 ATGGAAGAACTGTGATATTCGATTAATTT 67

RESULT 6

AAK61630/c

AAK61630/

19-JUN-1999 (first entry)

B. burgdorferi antigenic protein coding sequence, c739, nt.

Antigenic protein; vaccine; Lyme disease; infection; detection; ss.

Borrelia burgdorferi.

W09859071-A1.

30-DEC-1998.

18-JUN-1998; 98NC-0512718.

03-SEP-1997; 97US-0057483.

20-JUN-1997; 97US-0050359.

22-JUL-1997; 97US-0053377.

(HMDA) - HUMAN GENOME SCI INC.

(HMDA) - MEDIPONE INC.

Choi GH, Erwin AL, Hanson MS, Lathigra R;

NP1; 1999-189980/16.

P-PSDB; AAV19933.

Claim 1; Page 124; 275pp; English.

New isolated Borrelia burgdorferi nucleic acids - used to develop

product for the diagnosis, prevention and treatment of diseases

caused by Borrelia, particularly Lyme disease

CC This sequence encodes a Borrelia burgdorferi (Bb) protein of the

CC invention, which is suitable for use in a vaccine. The Bb polypeptides of

CC can be used in vaccines for eliciting protective antibodies to members of

CC the Borrelia genus, particularly for the use against Lyme disease in

CC humans and animals. They can be used for preventing or attenuating an

CC infection caused by a member of the Borrelia genus. The products can also

CC be used for detection of members of the Borrelia genus.

Sequence 615 BP; 212 A; 59 C; 98 G; 246 T; 0 other;

Query Match 69.7%; Score 21.6; DB 20; Length 615;

Best Local Similarity 88.7%; Pred. No. 1.6e02;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ATGGAAGAACTGTGATATTCGATTAATTT 28

DB 576 AATGGAAGAACTGTGATATTCGATTAATTT 549

RESULT 7

AAK61629/c

AAK61629/

19-JUN-1999 (first entry)

B. burgdorferi antigenic protein coding sequence, c739, nt.

Antigenic protein; vaccine; Lyme disease; infection; detection; ss.

Borrelia burgdorferi.

W09859071-A1.

30-DEC-1998.

18-JUN-1998; 98NC-0512718.

03-SEP-1997; 97US-0057483.

20-JUN-1997; 97US-0050359.

22-JUL-1997; 97US-0053377.

(HMDA) - HUMAN GENOME SCI INC.

(HMDA) - MEDIPONE INC.

Choi GH, Erwin AL, Hanson MS, Lathigra R;

NP1; 1999-189980/16.

P-PSDB; AAV19932.

New isolated Borrelia burgdorferi nucleic acids - used to develop

product for the diagnosis, prevention and treatment of diseases

caused by Borrelia, particularly Lyme disease

CC This sequence encodes a Borrelia burgdorferi (Bb) protein of the

CC invention, which is suitable for use in a vaccine. The Bb polypeptides of

CC can be used in vaccines for eliciting protective antibodies to members of

CC the Borrelia genus, particularly for the use against Lyme disease in

CC humans and animals. They can be used for preventing or attenuating an

CC infection caused by a member of the Borrelia genus. The products can also

CC be used for detection of members of the Borrelia genus.

Sequence 654 BP; 227 A; 61 C; 104 G; 262 T; 0 other;

Query Match 69.7%; Score 21.6; DB 20; Length 654;

Best Local Similarity 88.7%; Pred. No. 1.6e02;

Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 ATGGAAGAACTGTGATATTCGATTAATTT 28

615 AATGGAAGAACTGTGATATTCGATTAATTT 588

AAK60942/c

05-JUN-2001 (first entry)

Human digestive system antigen genomic sequence SRD ID NO. 4518.

human, digestive system antigen, gene therapy, cancer, appendicitis;

ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
digestive system disorder; Meckel's diverticulum; etc.

Homo sapiens.

WC000155314-M2.

02-ANG-2001.

17-JAN-2001, 2001NOV-080124.

31-JAN-2000, 2000JUN-019065.

04-FEB-2000, 2000JUN-0180628.

24-FEB-2000, 2000JUN-018466.

16-MAR-2000, 2000JUN-0189872.

17-MAR-2000, 2000JUN-019076.

18-APR-2000, 2000JUN-0198123.

07-JUN-2000, 2000JUN-0209467.

28-JUN-2000, 2000JUN-0214866.

30-JUN-2000, 2000JUN-0215135.

07-JUL-2000, 2000JUN-0216647.

11-JUL-2000, 2000JUN-0217887.

11-JUL-2000, 2000JUN-0217996.

14-JUL-2000, 2000JUN-0218299.

26-JUL-2000, 2000JUN-0220964.

14-AUG-2000, 2000JUN-0224518.

14-AUG-2000, 2000JUN-0224519.

14-AUG-2000, 2000JUN-0225211.

14-AUG-2000, 2000JUN-0225266.

14-AUG-2000, 2000JUN-0225267.

14-AUG-2000, 2000JUN-0225447.

14-AUG-2000, 2000JUN-0225457.

14-AUG-2000, 2000JUN-0225758.

14-AUG-2000, 2000JUN-0225758.

14-AUG-2000, 2000JUN-0225758.

22-AUG-2000, 2000JUN-0226868.

22-AUG-2000, 2000JUN-0227182.

30-AUG-2000, 2000JUN-0228924.

01-SEP-2000, 2000JUN-0229343.

01-SEP-2000, 2000JUN-0229344.

05-SEP-2000, 2000JUN-0229509.

05-SEP-2000, 2000JUN-0229513.

08-SEP-2000, 2000JUN-0231244.

08-SEP-2000, 2000JUN-0231244.

08-SEP-2000, 2000JUN-0231244.

25-SEP-2000, 2000JUN-0231997.

25-SEP-2000, 2000JUN-0231998.

27-SEP-2000, 2000JUN-0235834.

27-SEP-2000, 2000JUN-0235836.

28-SEP-2000, 2000JUN-0236327.

28-SEP-2000, 2000JUN-0236328.

29-SEP-2000, 2000JUN-0236358.

29-SEP-2000, 2000JUN-0236359.

29-SEP-2000, 2000JUN-0236370.

02-OCT-2000, 2000JUN-0237039.

02-OCT-2000, 2000JUN-0237039.

02-OCT-2000, 2000JUN-0237039.

13-OCT-2000, 2000JUN-0239937.

20-OCT-2000, 2000JUN-0241221.

20-OCT-2000, 2000JUN-0241221.

20-OCT-2000, 2000JUN-0241787.

20-OCT-2000, 2000JUN-0241787.

20-OCT-2000, 2000JUN-0241808.

20-OCT-2000, 2000JUN-0241809.

01-NOV-2000, 2000JUN-0244617.

08-NOV-2000, 2000JUN-0244617.

08-NOV-2000, 2000JUN-0244617.

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08-NOV-2000, 2000JUN-0244617.

08-NOV-2000, 2000JUN-0244617.









RESULT 11  
 AB90312  
 X1 AB90312 standard; DNA, 7737 BP.  
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XX cycloine methylation; de.  
XX Homo sapiens.

XX W020016932-1A3.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001MO-BE07955.

XX 15-MAR-2000; 2000DE-1013447.

XX 06-APR-2000; 2000DE-1013958.

XX 07-APR-2000; 2000DE-1013173.

XX 30-JUN-2000; 2000DE-1032523.

XX 01-SEP-2000; 2000DE-1043528.

XX (EPID) - EPIDEMIOLOGICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-602152/68.

XX Fragments of chemically modified genes associated with tumour suppressor

XX PT analyzing diseases associated with cycloine methylation state e.g.

XX cancer -

XX Claim 1, SEQ ID NO 139; 27pp; English.

XX The invention relates to a nucleic acid comprising a sequence of 18

XX bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with

XX bisulphite, of genes associated with tumour suppression and/or

XX numbers 408, 458 and 500 are missing from the sequence listing) sequences

XX (8s) and sequences complementary to (8s). The nucleic acid may be a

XX peptide nucleic acid-oligonucleotide (PNA) of at least 3 nucleotides and may

XX be a single nucleotide polymorphism and also to be used in an

XX array for analysing diseases associated with CpG dinucleotides e.g.

XX cancers and tumours. The probes can also be used in a method for

XX and/or therapy of diseases associated with CpG dinucleotides e.g.

XX diseases, by analysing cytosine methylations. The parameters may be

XX compared to another set of genotypic and/or epigenetic parameters, the

XX differences serving as basis for diagnosis and/or prognostic events which

XX are associated with the diseases. The parameters may be used in the

XX 533 genomic sequences derived from tumour suppressor genes and

XX complementary sequences with even numbered seq ID numbers are the

XX oncogenes. Sequences with odd numbered seq ID numbers are the

XX complementary sequence of the corresponding odd numbered sequence (e.g.

XX 18 missing), ID 538 and ID 539, except for those whose partner sequence

XX Note: The sequence data for this patent did not form part

XX of the printed specification, but was obtained in electronic

XX ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 13377 BP; 3714 A; 146 C; 2702 G; 6815 T; 0 other;

XX Query Match 69.7%; Score 21.6; DB 23; Length 13377;

XX Best Local Similarity 85.7%; Pred. No. 1.5e+02;

XX Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 4 GTGAAATTCGTGATTAATTAATTTT 31

XX 1827 GTGAAATTCGTGATTAATTAATTTT 1854

XX RESULT 13

XX ABL3463

XX ID ABL3463 standard; DNM; 13377 BP.

XX ABL3463;

XX

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 1436.

XX Human; immune system disease; cycloine methylation; antiaesthetic;

XX antiaesthetic; antiaesthetic; antiaesthetic; antiaesthetic;

XX antiaesthetic; antiaesthetic; antiaesthetic; antiaesthetic;

XX antiaesthetic; antiaesthetic; antiaesthetic; antiaesthetic;

XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

XX seq; de.

XX Homo sapiens.

XX W020020020-12.

XX 03-JAN-2002.

XX 02-JUL-2001; 2001MO-BE07557.

XX 30-JUN-2000; 2000DE-1032529.

XX 01-SEP-2000; 2000DE-1043266.

XX (EPID) - EPIDEMIOLOGICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-103090/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful

XX for diagnosis and treatment of diseases associated with abnormal

XX cytosine methylation

XX Claim 1, SEQ ID NO 1436; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated

XX genes, which can be used in the diagnosis and treatment of immune system disorders,

XX including eye diseases such as retinopathy, neovascular glaucoma and

XX macular degeneration, arteriosclerosis, anemias, cancer, acute myeloid

XX leukemia, rheumatoid arthritis, psoriasis and inflammatory/alcoholic bowel

XX disease. The present sequence is a gene of the invention.

XX Sequence 13377 BP; 3714 A; 146 C; 2702 G; 6815 T; 0 other;

XX Query Match 69.7%; Score 21.6; DB 24; Length 13377;

XX Best Local Similarity 85.7%; Pred. No. 1.5e+02;

XX Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 4 GTGAAATTCGTGATTAATTAATTTT 31

XX 1827 GTGAAATTCGTGATTAATTAATTTT 1854

XX RESULT 14

XX AAX20250

XX AAX20250 standard; DNM; 11109 BP.

XX AAX20250;

XX 04-MAY-1999 (first entry)

XX Borrelia burgdorferi polymucleotide sequence #3.

XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;

XX infection; Borrelia burgdorferi; Lyme disease; Lyme disease;



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 09:02:17 ; Search time 45.2295 Seconds  
(with about 315 comments)

302.521 Million cell

Sequence: 1 atagtgaaaactgtgtcaattatgaaattt 31

Gapop 10.0 , Gapext 2.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Minimum DB seq length: 0
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**Book** ————— **Mileage** **Rate** **Cash**

Post-processing: Minimum Match 0%  
Maximum Match 70%

Listing first 45 summaries

Database :

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1: /cgm2_6/ptodata/2/ina/5B_COMB.seg.*
2: /cgm2_6/ptodata/2/ina/5B_COMB.seg.*
3: /cgm2_6/ptodata/2/ina/6A_COMB.seg.*
4: /cgm2_6/ptodata/2/ina/6B_COMB.seg.*
5: /cgm2_6/ptodata/2/ina/PCITS_COMB.seg.*
6: /cgm2_6/ptodata/2/ina/backfillse1.seg.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | CCSN    | Query length | DB     | ID | Description       |
|------------|---------|--------------|--------|----|-------------------|
| 1          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 445, App |
| 2          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 446, App |
| 3          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 447, App |
| 4          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 448, App |
| 5          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 449, App |
| 6          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 450, App |
| 7          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 451, App |
| 8          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 452, App |
| 9          | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 453, App |
| 10         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 454, App |
| 11         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 455, App |
| 12         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 456, App |
| 13         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 457, App |
| 14         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 458, App |
| 15         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 459, App |
| 16         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 460, App |
| 17         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 461, App |
| 18         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 462, App |
| 19         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 463, App |
| 20         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 464, App |
| 21         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 465, App |
| 22         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 466, App |
| 23         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 467, App |
| 24         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 468, App |
| 25         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 469, App |
| 26         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 470, App |
| 27         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 471, App |
| 28         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 472, App |
| 29         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 473, App |
| 30         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 474, App |
| 31         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 475, App |
| 32         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 476, App |
| 33         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 477, App |
| 34         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 478, App |
| 35         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 479, App |
| 36         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 480, App |
| 37         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 481, App |
| 38         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 482, App |
| 39         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 483, App |
| 40         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 484, App |
| 41         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 485, App |
| 42         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 486, App |
| 43         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 487, App |
| 44         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 488, App |
| 45         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 489, App |
| 46         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 490, App |
| 47         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 491, App |
| 48         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 492, App |
| 49         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 493, App |
| 50         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 494, App |
| 51         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 495, App |
| 52         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 496, App |
| 53         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 497, App |
| 54         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 498, App |
| 55         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 499, App |
| 56         | 1, 9, 4 | 62, 6        | 1, 001 | 4  | Sequence 500, App |

## ALIGNMENTS

|   |    |      |      |         |                      |                   |
|---|----|------|------|---------|----------------------|-------------------|
| C | 28 | 18.4 | 59.4 | 5.00    | 4 US-09-126-523,-86  | Sequence 86, Appl |
| C | 29 | 18.4 | 59.4 | 5.00    | US-09-733-792A-86    | Sequence 86, Appl |
| C | 30 | 18.4 | 59.4 | 5.00    | US-08-431-148F-86    | Sequence 86, Appl |
| C | 31 | 18.4 | 59.4 | 5.00    | US-08-431-148F-86    | Sequence 86, Appl |
| C | 32 | 18.4 | 59.4 | 5.00    | US-09-123-352-255.1  | Sequence 255, Ap  |
| C | 33 | 18.4 | 59.4 | 1330025 | 4 US-09-126-452A-1   | Sequence 1, Appl  |
| C | 34 | 18.2 | 56.7 | 717.7   | 4 US-09-126-523-1778 | Sequence 1778, Ap |
| C | 35 | 18.2 | 56.7 | 1413.1  | US-07-365-982A-4     | Sequence 4, Appl  |
| C | 36 | 18.2 | 56.7 | 1456.4  | US-09-064-981A-23    | Sequence 23, Appl |
| C | 37 | 18.2 | 56.7 | 2539.3  | US-08-748-524-3      | Sequence 3, Appl  |
| C | 38 | 18.2 | 56.7 | 3199.4  | US-09-149-132A-3     | Sequence 3, Appl  |
| C | 39 | 18.2 | 56.7 | 4379.1  | US-08-552-125A-17    | Sequence 17, Appl |
| C | 40 | 18.2 | 56.7 | 4379.1  | US-09-143-976-17     | Sequence 17, Appl |
| C | 41 | 18.2 | 56.7 | 4379.1  | US-08-552-125A-17    | Sequence 17, Appl |
| C | 42 | 18.2 | 56.7 | 7210.2  | US-08-557-862B-10    | Sequence 10, Appl |
| C | 43 | 18.2 | 56.7 | 7210.2  | US-08-557-862B-10    | Sequence 10, Appl |
| C | 44 | 18.2 | 56.7 | 7210.2  | US-08-557-862B-10    | Sequence 10, Appl |
| C | 45 | 18.2 | 56.7 | 7210.2  | FCT-US95-0720A1-10   | Sequence 10, Appl |

ALIGNMENTS

```

RESULT 1
US-09-641-638-465/c
      / Sequence 465, Application US/0661638
      / Patent No. 6638468
      / Applicant: Biogenetec, Inc.
      / APPLICANT: Biogenetec, Inc.
      / APPLICANT: Biogenetec, Lytle
      / APPLICANT: Cumbuck, Ilya
      / TITLE OF INVENTION: RALPHATIC MARKERS DERIVED FROM GENOMIC REGIONS
      / FILE REFERENCE: GENET 051C1
      / CURRENT APPLICATION NUMBER: 06/09/641.638
      / PRIOR APPLICATION NUMBER: US 02/502.330
      / PRIOR FILING DATE: 2000-02-11
      / PRIOR APPLICATION NUMBER: US 60/133.200
      / PRIOR FILING DATE: 1999-05-01 09/75.267
      / PRIOR FILING DATE: 1999-03-23
      / PRIOR APPLICATION NUMBER: US 60/119.917
      / PRIOR FILING DATE: 1999-02-12
      / NUMBER OF SEQ ID NOS: 104
      / SEQ ID NO 465
      / SEQ ID NO 466
      / TYPE: DNA
      / ORGANISM: Homo Sapiens
      / NAME/KEY: allele
      / OTHER INFORMATION: 5'31
      / LOCATION: 501
      / OTHER INFORMATION: 12-44-50 : polymorphic base T or C
      / LOCATION: 502
      / OTHER INFORMATION: 12-44-50.mbl, potential complement
      / NAME/KEY: misc binding
      / LOCATION: 468..500
      / OTHER INFORMATION: 12-44-50.mbl2
      / NAME/KEY: primer bind
      / LOCATION: 530..550
      / OTHER INFORMATION: upstream amplification primer, complement
      / NAME/KEY: primer bind
      / LOCATION: 489..513
      / OTHER INFORMATION: downstream amplification primer
      / NAME/KEY: misc binding
      / LOCATION: 489..513
      / OTHER INFORMATION: 12-44-50 potential probe
      / US-09-641.638-465
Query Match          62.6%; Score 19.4; DB 4; length 1001;

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Best Local Similarity 79.3%; Pred. No. 1.1e+02;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Q# 2 TACGAAACCTGGTATATATGAAATTT 30  
DB 491 TACGAAACCTGGTATATATGAAATTT 519

RESULT 5  
US-09-687-147-1  
Sequence 1, Application US/09687147  
GENERAL INFORMATION:  
APPLICANT: Li, Xin-Liang  
APPLICANT: Chen, Huizong  
TITLE OF INVENTION: Novel databases and Coding Sequences  
FILE REFERENCE: 42-96a  
CURRENT APPLICATION NUMBER: US/09/687,147  
CURRENT FILING DATE: 2000-10-12  
PRIOR FILING DATE: 1996-10-04  
PRIOR APPLICATION NUMBER: PCT US97/18008  
PRIOR FILING DATE: 1997-10-03  
PRIOR FILING DATE: 1998-03-02  
PRIOR FILING DATE: 1999-04-05  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1568  
LOCUS: 1568  
TYPE: DNA  
ORGANISM: Oryzomyces sp. PC-2  
FEATURE: CDS  
LOCATION: (105)..(1481)  
US-09-687-147-1  
Query Match 62.6%; Score 19.4; DB 3;  
Best Local Similarity 79.3%; Pred. No. 1.1e+02;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Q# 2 TACGAAACCTGGTATATATGAAATTT 30  
DB 491 TACGAAACCTGGTATATATGAAATTT 519

RESULT 7  
US-09-539-333D-216/C  
Sequence 216, Application US/0953933D  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougaldec, Lydie  
APPLICANT: Beshkov, Laurent  
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIOMOLECULAR MARKERS  
FILE REFERENCE: GENEST 047AUS  
CURRENT APPLICATION NUMBER: US/09/539,333D  
CURRENT FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: US 60/126,903  
PRIOR FILING DATE: 1999-03-30  
PRIOR APPLICATION NUMBER: US 60/131,971  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: US 60/143,928  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: US 60/145,915  
PRIOR FILING DATE: 1999-07-27  
PRIOR APPLICATION NUMBER: US 60/146,453  
US-09-539-333D-117  
Query Match 62.6%; Score 19.4; DB 4;  
Best Local Similarity 79.3%; Pred. No. 1.1e+02;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Q# 3 AGCGAAACCTGGTATATATGAAATTT 31  
DB 2059 AGCGAAACCTGGTATATATGAAATTT 2031

RESULT 7  
US-09-539-333D-216/C  
Sequence 216, Application US/0953933D  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougaldec, Lydie  
APPLICANT: Beshkov, Laurent  
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIOMOLECULAR MARKERS  
FILE REFERENCE: GENEST 047AUS  
CURRENT APPLICATION NUMBER: US/09/539,333D  
CURRENT FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: US 60/126,903  
PRIOR FILING DATE: 1999-03-30  
PRIOR APPLICATION NUMBER: US 60/131,971  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: US 60/143,928  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: US 60/145,915  
PRIOR FILING DATE: 1999-07-27  
PRIOR APPLICATION NUMBER: US 60/146,453  
US-09-539-333D-117  
Query Match 62.6%; Score 19.4; DB 4;  
Best Local Similarity 79.3%; Pred. No. 1.1e+02;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Q# 3 AGCGAAACCTGGTATATATGAAATTT 31  
DB 2059 AGCGAAACCTGGTATATATGAAATTT 2031

```

PRIOE FILING DATE: 1999-07-29
PRIOE APPLICATION NUMBER: US 60/146,452
PRIOE PUBLICATION NUMBER: US 6,162,288
PRIOE FILING DATE: 1999-10-28
PRIOE APPLICATION NUMBER: US 09/416,384
PRIOE PUBLICATION NUMBER: US 6,999,112
NUMBER OF SEQ ID NOS: 211
SOFTWARE: Patent.pm
SEQ ID NO 216
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
OTHER INFORMATION: 99-27297-280 : polymorphic base T or C
FEATURE:
NAME/KEY: nasec binding
OTHER INFORMATION: 99-27297-280 : polymorphic base T or C
FEATURE:
NAME/KEY: nasec binding
OTHER INFORMATION: 99-27297-280 : m181,
FEATURE:
NAME/KEY: nasec binding
OTHER INFORMATION: 99-27297-280 : m182, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 1751..1779
FEATURE:
NAME/KEY: primer bind
LOCATION: 1206..1224
FEATURE:
NAME/KEY: primer bind
LOCATION: 1489..1513
FEATURE:
NAME/KEY: nasec binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-27297-280 : probe
US-99-35-3839-216

Query Match          62.6% Score 19.4; DB 4; Length 3001;
Basic Local Similarity 79.3%; Freq. No. 1.1e+02;
Matches 257 Complementary 0; Mismatched 6; Indels 0; Gaps 0;
QY 3 AGTGAAGACCTGCTGATTAATTAATTT 21
Db 2912 AGTGAAGACCTGCTGATTAATTAATTT 2884

PRIOE FILING DATE: 1999-07-29
PRIOE APPLICATION NUMBER: US 60/146,452
PRIOE PUBLICATION NUMBER: US 6,162,288
PRIOE FILING DATE: 1999-10-28
PRIOE APPLICATION NUMBER: US 09/416,384
PRIOE PUBLICATION NUMBER: US 6,999,112
NUMBER OF SEQ ID NOS: 211
SOFTWARE: Patent.pm
SEQ ID NO 1
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
OTHER INFORMATION: 99-27297-280 : polymorphic base T or C
FEATURE:
NAME/KEY: nasec binding
OTHER INFORMATION: 99-27297-280 : polymorphic base T or C
FEATURE:
NAME/KEY: nasec binding
OTHER INFORMATION: 99-27297-280 : m181,
FEATURE:
NAME/KEY: nasec binding
OTHER INFORMATION: 99-27297-280 : m182, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 1751..1779
FEATURE:
NAME/KEY: primer bind
LOCATION: 1206..1224
FEATURE:
NAME/KEY: primer bind
LOCATION: 1489..1513
FEATURE:
NAME/KEY: nasec binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-27297-280 : probe
US-99-35-3839-216

```

|                                |                                      |  |
|--------------------------------|--------------------------------------|--|
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| OTHER INFORMATION: 5-127-261   | : polymorphic base A or C            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| OTHER INFORMATION: 99-1437-325 | : polymorphic base A or G            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| OTHER INFORMATION: 5-128-60    | : polymorphic base deletion of GT    |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| OTHER INFORMATION: 99-1442-224 | : polymorphic base G or T            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 91132                | : polymorphic base deletion of T     |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 99098                | : polymorphic base A or G            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 99117                | : polymorphic base A or G            |  |
| OTHER INFORMATION: 5-130-276   | : polymorphic base A or C            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 103806               | : polymorphic base A or T            |  |
| OTHER INFORMATION: 5-131-395   | : polymorphic base insertion of A    |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 106540               | : polymorphic base insertion of A    |  |
| OTHER INFORMATION: 5-133-375   | : polymorphic base insertion of A    |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 108106               | : polymorphic base insertion of A    |  |
| OTHER INFORMATION: 5-135-155   | : polymorphic base insertion of GTTT |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 108149               | : polymorphic base A or G            |  |
| OTHER INFORMATION: 5-135-198   | : polymorphic base insertion of GTTT |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 108308               | : polymorphic base A or G            |  |
| OTHER INFORMATION: 5-135-357   | : polymorphic base C or T            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 108471               | : polymorphic base C or T            |  |
| OTHER INFORMATION: 5-136-174   | : polymorphic base C or T            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 134134               | : polymorphic base C or T            |  |
| OTHER INFORMATION: 5-140-120   | : polymorphic base C or T            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 134362               | : polymorphic base insertion of A    |  |
| OTHER INFORMATION: 5-140-348   | : polymorphic base insertion of A    |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| LOCATION: 134472               | : polymorphic base insertion of CA   |  |
| OTHER INFORMATION: 5-140-361   | : polymorphic base insertion of CA   |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| OTHER INFORMATION: 5-143-84    | : polymorphic base A or G            |  |
| NAME/KEY: a11a1e               | FEATURE:                             |  |
| OTHER INFORMATION: 5-143-101   | : polymorphic base A or C            |  |





TELEPHONE: (415) 324-0800  
 TELEFAX: (415) 324-0650  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14855 base pairs  
 TYPE: Linear  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 RECOMBINATION: NO  
 REFERENCES: 1  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATES: 5' END OF INTERON 2 OF RAD50 GENOMIC  
 US-09-889-490-55

Query Match 61.3%; Score 19; DB 2; Length 14855;  
 Best Local Similarity 81.5%; Pred. No. 1.4e+02;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

5 TGAAGAACTGTGGATTAATGAAATTT 31  
 355 TGAACCTTTCATGAGTATGATGAAATTT 381

RESULT 10  
 PCT-US96-07709-18  
 GENERAL INFORMATION:

APPLICANT: wisniewski, Nancy  
 TITLE OF INVENTION: PARASITIC HELMINTH YENON ALLERGEN  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSER: Sheridan Ross & McIntosh  
 STREET: 1700 Lincoln St., Suite 3500  
 CITY: Denver  
 STATE: Colorado  
 COUNTRY: U.S.A.  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 SOFTWARE: GENES 5-LIKE GENES AND PROTEINS  
 CURRENT APPLICATION DATA: PCT/US96/07709  
 FILING DATE: 23-MAY-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Connell, Gary J.  
 REGISTRATION NUMBER: 12,020  
 TELEPHONE: (303) 863-9700  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 863-9700  
 INVENTOR: WISNIEWSKI, NANCY  
 LENGTH: 594 base pairs  
 TYPE: nucleic acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 FEATURES:  
 NAME/KEY: CDS  
 DEFINITION: CDS  
 LOCATION: 1..593

Query Match 60.4%; Score 18.8; DB 5; Length 594;  
 Best Local Similarity 76.7%; Pred. No. 1.9e+02;  
 Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 AATGTAATACCTGTGATTAATGAAATTT 30  
 12 AATGTAATACCTGTGATTAATGAAATTT 41

RESULT 11  
 PCT-US96-07709-20/6

GENERAL INFORMATION:  
 Sequence 20, Application PCT/US9607709  
 APPLICANT: TTPP, Cynthia A.  
 TITLE OF INVENTION: PARASITIC HELMINTH YENON ALLERGEN  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSER: Sheridan Ross & McIntosh  
 STREET: 1700 Lincoln St., Suite 3500  
 CITY: Denver  
 STATE: Colorado  
 COUNTRY: U.S.A.  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 SOFTWARE: GENES 5-LIKE GENES AND PROTEINS  
 CURRENT APPLICATION DATA: PCT/US96/07709  
 FILING DATE: 23-MAY-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Connell, Gary J.  
 REGISTRATION NUMBER: 12,020  
 TELEPHONE: (303) 863-9700  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 863-9700  
 INVENTOR: WISNIEWSKI, NANCY  
 LENGTH: 594 base pairs  
 TYPE: nucleic acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA

Query Match 60.6%; Score 18.8; DB 5; Length 594;  
 Best Local Similarity 76.7%; Pred. No. 1.9e+02;  
 Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 AATGTAATACCTGTGATTAATGAAATTT 30  
 583 AATGTAATACCTGTGATTAATGAAATTT 554

RESULT 12  
 PCT-US96-07709-27

GENERAL INFORMATION:  
 Sequence 27, Application PCT/US9607709  
 APPLICANT: TTPP, Cynthia A.  
 TITLE OF INVENTION: PARASITIC HELMINTH YENON ALLERGEN  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSER: Sheridan Ross & McIntosh  
 STREET: 1700 Lincoln St., Suite 3500  
 CITY: Denver  
 STATE: Colorado  
 COUNTRY: U.S.A.  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION NUMBER: PCT/US96/07709  
 FILING DATE: 23-MAY-1996  
 CLASSIFICATION INFORMATION:  
 APPLICANT/AGENT INFORMATION:  
 NAME: Cornell, Gary J.  
 REGISTRATION NUMBER: 32,020  
 REFERENCE/DOCKET NUMBER: 2618-30-PCT  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 27:  
 SOURCE CHARACTERISTICS:  
 TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS  
 TYPE: nucleic acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 PCT-US96-07709-27

Query Match 60.6%, Score 18.8, DB 5, Length 744,  
 Best Local Similarity 76.7%, Field No. 1-9e+02,  
 Matches 23, Conservative 0, Mismatches 7, Indels 0, Gaps 0,  
 Oy 1 ATGTGAAACCTGGATATGAAATTT 30  
 DB 10 AAGAGAACCTGGATATGAAATTT 39

RESULT 13  
 Sequence 28, Application PC/TUS9607709  
 GENERAL INFORMATION:  
 APPLICANT: Minswek, Henry  
 TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS: Rose & McIntosh  
 STREET: 1700 Lincoln St., Suite 3500  
 CITY: Denver  
 STATE: Colorado  
 ZIP: 80203  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 CONTAINER: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: PCT/US96/07709  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cornell, Gary J.  
 REGISTRATION NUMBER: 32,020  
 REFERENCE/DOCKET NUMBER: 2618-30-PCT  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 28:  
 SOURCE CHARACTERISTICS:  
 LENGTH: 744 base pairs  
 TYPE: nucleic acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 PCT-US96-07709-28

Query Match 60.6%, Score 18.8, DB 5, Length 744,  
 Best Local Similarity 76.7%, Field No. 1-9e+02,  
 Matches 23, Conservative 0, Mismatches 7, Indels 0, Gaps 0,  
 Oy 1 ATGTGAAACCTGGATATGAAATTT 30  
 DB 735 AAGAGAACCTGGATATGAAATTT 706

RESULT 14  
 Sequence 28, Application PC/TUS9607709  
 GENERAL INFORMATION:  
 APPLICANT: Minswek, Henry  
 TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS: Rose & McIntosh  
 STREET: 1700 Lincoln St., Suite 3500  
 CITY: Denver  
 STATE: Colorado  
 ZIP: 80203  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 CONTAINER: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: PCT/US96/07709  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cornell, Gary J.  
 REGISTRATION NUMBER: 32,020  
 REFERENCE/DOCKET NUMBER: 2618-30-PCT  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 29:  
 SOURCE CHARACTERISTICS:  
 LENGTH: 905 base pairs  
 TYPE: nucleic acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 FEATURE:  
 NAME/ENV: CDS  
 LOCATION: 1..749  
 PCT-US96-07709-24

Query Match 60.6%, Score 18.8, DB 5, Length 905,  
 Best Local Similarity 76.7%, Field No. 1-9e+02,  
 Matches 23, Conservative 0, Mismatches 7, Indels 0, Gaps 0,  
 Oy 1 ATGTGAAACCTGGATATGAAATTT 30  
 DB 12 AAGAGAACCTGGATATGAAATTT 41

RESULT 15  
 Sequence 28, Application PC/TUS9607709  
 GENERAL INFORMATION:  
 APPLICANT: Minswek, Henry  
 TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS: Rose & McIntosh  
 STREET: 1700 Lincoln St., Suite 3500  
 CITY: Denver  
 STATE: Colorado  
 ZIP: 80203  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 CONTAINER: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: PCT/US96/07709  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cornell, Gary J.  
 REGISTRATION NUMBER: 32,020  
 REFERENCE/DOCKET NUMBER: 2618-30-PCT  
 TELEPHONE: (303) 863-9700  
 TELEFAX: (303) 863-0223  
 INFORMATION FOR SEQ ID NO: 30:  
 SOURCE CHARACTERISTICS:  
 LENGTH: 905 base pairs  
 TYPE: nucleic acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 FEATURE:  
 NAME/ENV: CDS  
 LOCATION: 1..749  
 PCT-US96-07709-25

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/ STREET: 1700 Lincoln St., Suite 3500
/ CITY: Denver
/ STATE: Colorado
/ COUNTRY: U.S.A.
/ ZIP: 80203
/ COMPUTER READABLE FORM:
/ PATENT NUMBER: 5,828,829
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ COUNTRY: U.S.A.
/ APPLICATION NUMBER: PCT/US96/07709
/ FILING DATE: 23-MAY-1996
/ CLASSIFICATION:
/ AINVENT/AGENT INFORMATION:
/ NAME: Kernal 1.02
/ REGISTRATION NUMBER: 32,020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 863-0223
/ TELEFAX: (303) 863-0223
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 905 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE: cDNA
/ PCT-US96-07709-26
/
Query Match 60.6%; Score 18.8; DB 5; Length 905;
Base Local Similarity 70.7%; Pctd No. 8e+02;
Matches 2; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGTGAAACTGTGTATTTGAAATTT 30
DB 894 AAGGTGACGCTCTCTTATTCAGTATTT 865

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Search completed: December 18, 2003, 09:04:20  
 Job time : 50.2295 secs



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US-10-311-455-1946/C
Sequence 1946, Application US/10311455
GENERAL INFORMATION
APPLICANT: OLEK, Alexander
APPLICANT: PIENHSEBCK, Christian
TITLE OF INVENTION: Nucleic acids associated with the immune system by detect
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: PCT/EP01/07337
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032523.7
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1946
LENGTH: 7771
TYPE: DNA
ORGANISM: Artificial Sequence
GENERAL INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1946
Query Match 74.2% Score 23, DB 13, Length 7771,
Base Local Similarity 74%, Pred.No. 1e+02,
Matches 26, Conservative 0, Mismatches 5, Indels 0, Gaps 0,
DB 3122 AATTGGAACTTGTGTAATTCGAAATTT 31
4 ATGAGAACTTGTGTAATTCGAAATTT 31
US-09-878-574-8312
Sequence 8312, Application US/09878574
Patent No. US2002010548A1
GENERAL INFORMATION
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: PCT/US00/0878574
CURRENT FILING DATE: 2001-12-21
CURRENT APPLICATION NUMBER: US/09/878.574
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US/99/353.535
NUMBER OF SEQ ID NOS: 15972
SEQ ID NO 8312
LENGTH: 134
TYPE: DNA
ORGANISM: Glycine max
GENERAL INFORMATION:
US-09-878-574-8312
Query Match 72.8% Score 22.6, DB 10, Length 134,
Base Local Similarity 86.2%, Pred.No. 1e+02,
Matches 25, Conservative 4, Mismatches 4, Indels 0, Gaps 0,
DB 39 TATGTAATTCGTAATTCGTAATTCGTAATTT 30
4 TATGTAATTCGTAATTCGTAATTT 30
US-09-764-887-453
Sequence 453, Application US/09764887
GENERAL INFORMATION
APPLICANT: ROSEN, et al.
TITLE OF INVENTION: Nucleic Acid, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: US/09/764.887
PRIOR FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 638
SEQ ID NO 453
LENGTH: 7737
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-887-453
Query Match 69.7% Score 21.6, DB 9, Length 7737,
Base Local Similarity 7%, Pred.No. 4e+02,
Matches 24, Conservative 4, Mismatches 4, Indels 0, Gaps 0,
DB 4085 GTGAAACATTCGTAATTCGTAATTT 412
4 GTGAAACATTCGTAATTCGTAATTT 31
US-10-092-154-2001
Sequence 2001, Application US/10092154
Patent No. US2002012767A1
GENERAL INFORMATION
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCT/US00/092154
CURRENT FILING DATE: 2000-09-07
CURRENT APPLICATION NUMBER: US/10/092.154
NUMBER OF SEQ ID NOS: 2003
PRIOR FILING DATE: 2000-09-07
Prior application removed - See file wrapper or Palm
SEQ ID NO 2001
LENGTH: 7737
TYPE: DNA
ORGANISM: Homo sapiens
US-10-092-154-2001
Query Match 69.7% Score 21.6, DB 15, Length 7737,
Base Local Similarity 86.2%, Pred.No. 4e+02,
Matches 24, Conservative 4, Mismatches 4, Indels 0, Gaps 0,
DB 4085 GTGAAACATTCGTAATTCGTAATTT 412
4 GTGAAACATTCGTAATTCGTAATTT 31
US-09-764-847-2001
Sequence 2001, Application US/09764847
Patent No. US2002012767A1
GENERAL INFORMATION
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCT/US00/09764847
CURRENT FILING DATE: 2001-01-17
CURRENT APPLICATION NUMBER: US/09/764.847
PRIOR FILING DATE: 2000-09-07
Prior application removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SEQ ID NO 2001
LENGTH: 7737
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-847-2001
Query Match 69.7% Score 21.6, DB 10, Length 7737,
Base Local Similarity 85.7%, Pred.No. 4e+02,
Matches 24, Conservative 4, Mismatches 4, Indels 0, Gaps 0,
DB 4085 GTGAAACATTCGTAATTCGTAATTT 412
4 GTGAAACATTCGTAATTCGTAATTT 31
US-10-092-154-2001
Sequence 2001, Application US/10092154
Patent No. US2002012767A1
GENERAL INFORMATION
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCT/US00/092154
CURRENT FILING DATE: 2000-09-07
CURRENT APPLICATION NUMBER: US/10/092.154
NUMBER OF SEQ ID NOS: 2003
PRIOR FILING DATE: 2000-09-07
Prior application removed - See file wrapper or Palm
SEQ ID NO 2001
LENGTH: 7737
TYPE: DNA
ORGANISM: Homo sapiens
US-10-092-154-2001
Query Match 69.7% Score 21.6, DB 15, Length 7737,
Base Local Similarity 86.2%, Pred.No. 4e+02,
Matches 24, Conservative 4, Mismatches 4, Indels 0, Gaps 0,
DB 4085 GTGAAACATTCGTAATTCGTAATTT 412
4 GTGAAACATTCGTAATTCGTAATTT 31

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09 4 GCGAAGCTGGTGGATTTATGAAATTT 31  
 DB 4095 GCGAAGCTGGTGGATTTATGAAATTT 4142

RESULT 7  
 US-09-889-491-14  
 Sequence 453, Application US/10073961  
 Publication No. US2003007602A1  
 GENERAL INFORMATION: 1)  
 APPLICATION NUMBER: 60/225,447  
 TITLE REFERENCE: Polycl. Nucleic Acids, Proteins, and Antibodies  
 CURRENT FILING DATE: 2000-09-05  
 PRIOR FILING DATE: 2001-01-17, 60/187, 687  
 PRIOR APPLICATION NUMBER: 60/179, 065  
 PRIOR FILING DATE: 2000-01-31, 180, 428  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: 60/214, 886  
 PRIOR FILING DATE: 2000-06-28  
 PRIOR APPLICATION NUMBER: 60/217, 487  
 PRIOR FILING DATE: 2000-08-14  
 PRIOR APPLICATION NUMBER: 60/220, 963  
 PRIOR FILING DATE: 2000-07-11, 496  
 PRIOR APPLICATION NUMBER: 60/225, 447  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: 60/218, 290  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: 60/225, 757  
 PRIOR FILING DATE: 2000-08-22, 868  
 PRIOR APPLICATION NUMBER: 60/216, 647  
 PRIOR FILING DATE: 2000-07-07, 225, 270  
 PRIOR FILING DATE: 2000-08-14  
 PRIOR APPLICATION NUMBER: 60/216, 880  
 PRIOR FILING DATE: 2000-07-07, 225, 270  
 PRIOR FILING DATE: 2000-08-14  
 PRIOR APPLICATION NUMBER: 60/251, 869  
 PRIOR FILING DATE: 2000-12-08  
 PRIOR APPLICATION NUMBER: 60/235, 894  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: 60/234, 274  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: 60/228, 924  
 PRIOR FILING DATE: 2000-08-30  
 PRIOR APPLICATION NUMBER: 60/224, 518  
 PRIOR FILING DATE: 2000-08-16, 236, 369  
 PRIOR FILING DATE: 2000-09-29  
 PRIOR APPLICATION NUMBER: 60/224, 519  
 PRIOR FILING DATE: 2000-07-26, 964  
 PRIOR APPLICATION NUMBER: 60/241, 809  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR FILING DATE: 2000-11-27, 249, 289  
 PRIOR APPLICATION NUMBER: 60/236, 327  
 PRIOR FILING DATE: 2000-09-29  
 PRIOR APPLICATION NUMBER: 60/241, 785

PRIOR FILING DATE: 2000-10-20  
 PRIOR FILING DATE: 2000-06-24, 617  
 PRIOR FILING DATE: 2000-11-01, 268  
 PRIOR APPLICATION NUMBER: 60/225, 268  
 PRIOR FILING DATE: 2000-08-14  
 PRIOR APPLICATION NUMBER: 60/216, 368  
 PRIOR FILING DATE: 2000-09-29  
 PRIOR APPLICATION NUMBER: 60/251, 886  
 PRIOR FILING DATE: 2000-12-08  
 PRIOR APPLICATION NUMBER: 60/235, 894  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: 60/234, 274  
 PRIOR FILING DATE: 2000-09-01  
 PRIOR APPLICATION NUMBER: 60/234, 997  
 PRIOR FILING DATE: 2000-09-05, 343  
 PRIOR FILING DATE: 2000-09-01  
 PRIOR APPLICATION NUMBER: 60/229, 345  
 PRIOR FILING DATE: 2000-09-01  
 PRIOR APPLICATION NUMBER: 60/229, 287  
 PRIOR FILING DATE: 2000-09-01  
 PRIOR APPLICATION NUMBER: 60/233, 513  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 60/237, 039  
 PRIOR FILING DATE: 2000-09-05  
 PRIOR APPLICATION NUMBER: 60/237, 039  
 PRIOR FILING DATE: 2000-10-02  
 PRIOR APPLICATION NUMBER: 60/237, 038  
 PRIOR FILING DATE: 2000-09-29  
 PRIOR APPLICATION NUMBER: 60/236, 370  
 PRIOR FILING DATE: 2000-09-29  
 PRIOR APPLICATION NUMBER: 60/237, 037  
 PRIOR FILING DATE: 2000-10-02  
 PRIOR APPLICATION NUMBER: 60/237, 040  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/240, 960  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/239, 935  
 PRIOR FILING DATE: 2000-10-13  
 PRIOR APPLICATION NUMBER: 60/241, 787  
 PRIOR FILING DATE: 2000-10-20  
 PRIOR APPLICATION NUMBER: 60/246, 474  
 PRIOR FILING DATE: 2000-11-08  
 PRIOR APPLICATION NUMBER: 60/246, 532  
 PRIOR FILING DATE: 2000-11-08  
 PRIOR APPLICATION NUMBER: 60/249, 216  
 PRIOR FILING DATE: 2000-11-17  
 PRIOR APPLICATION NUMBER: 60/249, 210  
 PRIOR FILING DATE: 2000-08-14  
 PRIOR APPLICATION NUMBER: 60/228, 924  
 PRIOR FILING DATE: 2000-08-22, 182  
 PRIOR FILING DATE: 2000-08-22, 182  
 PRIOR APPLICATION NUMBER: 60/225, 214  
 PRIOR FILING DATE: 2000-08-14, 836  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: 60/230, 438  
 PRIOR FILING DATE: 2000-09-06, 213, 135  
 PRIOR FILING DATE: 2000-06-30

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PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,208
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,212
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,207
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,245
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,244
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,217
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/232,297
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/232,400
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/231,242
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,080
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,264
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,064
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,063
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,389
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08

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Query Match 69.7% Score 21.6; DB 15; Length 7737;
Sequence Similarity 0.02502407549
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 4 GCGAAACTCTGTATATATGAAATTT 31
Db 4085 GCGAACTCTGTATATATGAAATTT 4112

```

RESULT 8

```

US-10-311-455-1436
Sequence 1436; Application US/10311455
Publication No. US2003013506A1
Applicant: CURE, Alexander
Applicant: EISENBERG, Christian
Applicant: BERLIN, Kurt
Title of Invention: Cycloasine methylation
Associated with the Immune System by de
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032329.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1436
US-10-311-455-1436
TYPE: DNA
ORGANISM: Artificial Sequence
FUNCTION: INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1436

```

```

Query Match 69.7% Score 21.6; DB 13; Length 13377;
Sequence Similarity 0.02502407549
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 4 GCGAAACTCTGTATATATGAAATTT 31
Db 1827 GCGAACTCTGTATATATGAAATTT 1854

```

```

RESULT 9
US-10-311-455-1436
Sequence 213232; Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION: 14.0
APPLICANT: EISENBERG, Christian
TITLE OF INVENTION: Polymorphism in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/189,676
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PatsSeq for Windows Version 4.0
SEQ ID NO 1436
US-10-311-455-1436
TYPE: DNA
ORGANISM: Human
US-10-027-632-213232

```

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Query Match 69.0% Score 21.4; DB 13; Length 653;
Sequence Similarity 80.6% Pred. No. 3,48+02;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 AATGGGAAACTCTGGATTATGAAATTTT 31  
DB 486 AATGGGAACTCTGGATTATGAAATTTT 516

RESULT 10  
US-10-027-633-213232  
Sequence 33, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
CURRENT APPLICATION NUMBER: US/10/027,632  
PRIOR FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-26/01/85,218  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-26/01/56,358  
PRIOR FILING DATE: 1999-09-28/01/46,002  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 144  
SOFTWARE: PERL  
SEQ ID NO 213232  
LENGTH: 653  
ORGANISM: Human

Query Match 69.0%; Score 21.4; DB 14; Length 653;  
Best Local Similarity 80.6%; Pred. No. 4,46+02;  
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATGGGAAACTCTGGATTATGAAATTTT 31  
DB 486 AATGGGAACTCTGGATTATGAAATTTT 516

RESULT 11  
US-09-795-669-1371  
Sequence 1371, Application US/10106698  
GENERAL INFORMATION:  
APPLICANT: Steinhilber, Valgerdur  
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
FILE REFERENCE: P00051  
CURRENT APPLICATION NUMBER: US/10/106,698  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/157,137  
PRIOR FILING DATE: 1999-09-29/60/163,280  
PRIOR APPLICATION NUMBER: US 60/157,137  
PRIOR FILING DATE: 1999-11-02  
NUMBER OF SEQ ID NOS: 8564  
SOFTWARE: PatentIn Ver. 3.0  
SEQ ID NO 1371  
LENGTH: 2704  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
LOCATION: (1438)..  
OTHER INFORMATION: n equals a, t, g, or c  
US-10-106-698-1371

Query Match 69.0%; Score 21.4; DB 15; Length 2704;  
Best Local Similarity 80.6%; Pred. No. 4,46+02;  
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATGGGAAACTCTGGATTATGAAATTTT 31  
DB 966 AATGGGAACTCTGGATTATGAAATTTT 996

RESULT 12  
US-10-071-766-33  
Sequence 33, Application US/10071766  
GENERAL INFORMATION:  
APPLICANT: Chen  
TITLE OF INVENTION: GENES EXPRESSED IN SNEBSCENCE  
FILE REFERENCE: PA-0043 US  
CURRENT APPLICATION NUMBER: US/10/071,766  
PRIOR FILING DATE: 2002-02-07  
NUMBER OF SEQ ID NOS: 144  
SOFTWARE: PERL Program  
SEQ ID NO 33  
LENGTH: 3747  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
LOCATION: 3223-3355  
OTHER INFORMATION: a, t, c, g, or other  
US-10-071-766-33

Query Match 69.0%; Score 21.4; DB 14; Length 3747;  
Best Local Similarity 80.6%; Pred. No. 4,46+02;  
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATGGGAAACTCTGGATTATGAAATTTT 31  
DB 2026 AATGGGAACTCTGGATTATGAAATTTT 2056

RESULT 13  
US-09-795-669-1/C  
Sequence 1, Application US/09795668  
GENERAL INFORMATION:  
APPLICANT: Steinhilber, Valgerdur  
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE  
FILE REFERENCE: 2345,2004-001  
CURRENT APPLICATION NUMBER: US/09/795,668  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: US 09/515,716  
NUMBER OF SEQ ID NOS: 1531  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1503441  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: misc feature  
LOCATION: (1)..  
OTHER INFORMATION: F-G or A  
NAME/KEY: misc feature  
LOCATION: (11)..  
OTHER INFORMATION: Y=C/T or C  
NAME/KEY: misc feature  
LOCATION: (11)..  
OTHER INFORMATION: em or c  
US-09-795-669-1/C



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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=a or c or l/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or l/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or l/u
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or l/u
US-09-946-807-1

Query Match 69.0%; Score 21.4; DB 10; Length 1503841;
Best Local Similarity 80.6%; Pred. No. 9.5e+02;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 1 AATGCTAATAACTGTGTGTAATATTCAGAAATTTT 31
Db 567651 AATGCTAATAACTGTGTGTAATATTCAGAAATTTT 567621

```

Search completed: December 18, 2003, 10:23:13  
 Job time : 1014.1 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK nucleic - nucleic search using sw model

Run on: December 18, 2003, 09:02:17 Search time 3/76.39 seconds

File: us-09-889-491-14

Perfect score: 3

Sequence: 1 atcgagcaacttgcgaatgaatttt 31

Scoring table: IDENTITY, NTC

Gap: 16/0, Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 43562704

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximal Match 100%

Listing first 45 summaries

Database:

1: em.cebha:\*

2: em.cebha:\*

3: em.cebha:\*

4: em.cebha:\*

5: em.cebha:\*

6: em.cebha:\*

7: em.cebha:\*

8: em.cebha:\*

9: gb.ceb1:\*

10: gb.ceb1:\*

11: gb.ceb1:\*

12: gb.ceb1:\*

13: gb.ceb1:\*

14: gb.ceb1:\*

15: gb.ceb1:\*

16: gb.ceb1:\*

17: gb.ceb1:\*

18: gb.ceb1:\*

19: gb.ceb1:\*

20: gb.ceb1:\*

21: gb.ceb1:\*

22: gb.ceb1:\*

23: gb.ceb1:\*

24: gb.ceb1:\*

25: gb.ceb1:\*

26: gb.ceb1:\*

27: gb.ceb1:\*

28: gb.ceb1:\*

29: gb.ceb1:\*

30: gb.ceb1:\*

31: gb.ceb1:\*

32: gb.ceb1:\*

33: gb.ceb1:\*

34: gb.ceb1:\*

35: gb.ceb1:\*

36: gb.ceb1:\*

37: gb.ceb1:\*

38: gb.ceb1:\*

39: gb.ceb1:\*

40: gb.ceb1:\*

41: gb.ceb1:\*

42: gb.ceb1:\*

43: gb.ceb1:\*

44: gb.ceb1:\*

45: gb.ceb1:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a  
score of the same or higher than the score of the result being printed,  
and is derived by analysis of the total score distribution.

| Result No. | Score | Match | Length | DB ID   | Description      |
|------------|-------|-------|--------|---------|------------------|
| 1          | 24.6  | 79.4  | 850    | CC08689 | CC08689 CSU-K33- |
| 2          | 24.6  | 79.4  | 850    | CC08689 | CC08689 CSU-K33- |
| 3          | 24.6  | 79.4  | 850    | CC08689 | CC08689 CSU-K33- |
| 4          | 24.6  | 79.4  | 850    | CC08689 | CC08689 CSU-K33- |

|    |      |      |     |         |                  |
|----|------|------|-----|---------|------------------|
| 5  | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 6  | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 7  | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 8  | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 9  | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 10 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 11 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 12 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 13 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 14 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 15 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 16 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 17 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 18 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 19 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 20 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 21 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 22 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 23 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 24 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 25 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 26 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 27 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 28 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 29 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 30 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 31 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 32 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 33 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 34 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 35 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 36 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 37 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 38 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 39 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 40 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 41 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 42 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 43 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 44 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |
| 45 | 24.6 | 79.4 | 850 | CC08689 | CC08689 CSU-K33- |

## ALIGNMENTS

CC08689 3436-67 CSU-K33-3436-67 genomic survey sequence.  
DEFINITION  
CC08689.1 GI:2944434

Accession  
CC08689.1

Version  
CC08689.1

Source  
CC08689.1

Organism  
CC08689.1

Reference  
CC08689.1

Authors  
CC08689.1

Title  
CC08689.1

Journal  
CC08689.1

Comment  
CC08689.1

Seq primary: 17

Department of Eukaryotic Genomics

300 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: emce@fcr.org

State University

Seq primary: 17

Class: BAC ends.  
Location/Qualifiers  
SOURCE  
1. .181.gsm::Aedes aegypti\*  
/mol type="genomic DNA"  
/db xref="taxon:7159"  
/strain="Rexy111c"  
/organism="Aedes aegypti"  
/clone .1lb="CSU-K33r.34G16"  
/note="Vector: pBeloExcl1, Site.1: HindIII"

BASE COUNT  
48 a 79 48  
16 c 51 g 66 t

ORIGIN

Query Match 79.4%; Score 24.6; DB 29; Length 181;  
Best Local Similarity 87.1%; Pred. No. 1.7e+02;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR 1 ATGTGAAACCTGTGATTTGAAATTTT 31  
32 ATGTGAAACCTGTGATTTGAAATTTT 62

RESULT 2  
CC088678/c 242 bp DNA linear GSS 16-APR-2003  
DEFINITION  
CSU-K33r.34G16, spmc CSU-K33r Aedes aegypti genomic clone  
ACCESSION  
CC088678  
VERSION  
CC088678.1 GI:29944112  
SOURCE  
Rexy111c  
ORGANISM  
Aedes aegypti (yellow fever mosquito)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
1 base 1 to 242; protein, dipetala; Neomecozoa; Culicoidae; Aedes.  
Loftus B., Shetty, J., Severson, D., Brown, S. and Knudson, D.  
has sequencing of Aedes aegypti BACs  
Other GSSs: CSU-K33r.34G16.T7  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: ems@ncsl.org  
Library was provided by Susan Brown and Dennis Knudson at Colorado State University.  
Seq primer: SPE  
Class: BAC ends  
Location/Qualifiers  
/organism="Aedes aegypti"  
/mol type="genomic DNA"  
/db xref="taxon:7159"  
/strain="Rexy111c"  
/clone .1lb="CSU-K33r.34G16"  
/note="Vector: pBeloExcl1, Site.1: HindIII"

BASE COUNT  
79 a 79 48  
16 c 51 g 66 t

ORIGIN

Query Match 79.4%; Score 24.6; DB 29; Length 242;  
Best Local Similarity 87.1%; Pred. No. 1.7e+02;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR 1 ATGTGAAACCTGTGATTTGAAATTTT 31  
116 ATGTGAAACCTGTGATTTGAAATTTT 86

LOCUS  
CC115662 537 bp DNA linear GSS 16-APR-2003  
DEFINITION  
NDL-35011.T7 Noire Dame Liverpool Aedes aegypti genomic clone  
ACCESSION  
CC115662  
VERSION  
CC115662.1 GI:2994617  
SOURCE  
GSS  
KEYWORDS  
Aedes aegypti (yellow fever mosquito)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
1 base 1 to 537; protein, dipetala; Neomecozoa; Culicoidae; Aedes.  
Loftus B., Shetty, J., Severson, D., Brown, S. and Knudson, D.  
has sequencing of Aedes aegypti BACs  
Other GSSs: CSU-K33r.15020.8P6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: ems@ncsl.org  
Library was provided by David Severson  
Seq primer: 17  
Class: BAC ends  
Location/Qualifiers  
/organism="Aedes aegypti"  
/mol type="genomic DNA"  
/db xref="taxon:7159"  
/strain="Rexy111c"  
/clone .1lb="Noire Dame Liverpool"  
/note="Vector: pBeloExcl1, Site.1: Hind III, The library was  
provided by David Severson at the University of Notre Dame and  
Hongbin Zhang"

BASE COUNT  
147 a 67 c 161 g 162 t

ORIGIN

Query Match 79.4%; Score 24.6; DB 29; Length 537;  
Best Local Similarity 87.1%; Pred. No. 2.1e+02;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR 1 ATGTGAAACCTGTGATTTGAAATTTT 31  
40 ATGTGAAACCTGTGATTTGAAATTTT 70

RESULT 4  
CC074394 696 bp DNA linear GSS 16-APR-2003  
DEFINITION  
CSU-K33r.15020.T7 CSU-K33r Aedes aegypti genomic clone  
ACCESSION  
CC074394  
VERSION  
CC074394.1 GI:2915019  
SOURCE  
GSS  
KEYWORDS  
Aedes aegypti (yellow fever mosquito)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
1 base 1 to 696; protein, dipetala; Neomecozoa; Culicoidae; Aedes.  
Loftus B., Shetty, J., Severson, D., Brown, S. and Knudson, D.  
has sequencing of Aedes aegypti BACs  
Other GSSs: CSU-K33r.15020.8P6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: ems@ncsl.org  
Library was provided by Susan Brown and Dennis Knudson at Colorado





Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84142, USA 8606  
 Email: edmundgenetics@utah.edu  
 Phone: 801 585 7177  
 Fax: 801 585 7177  
 Insert length: 10000 Std Error: 0.00  
 Primer: 6180 Rev: 1 column: 02  
 Primer: 6180 Rev: 1 column: 02  
 Class: Plasmid ends  
 High quality sequence stop: 616.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /strain="CEB76/67"  
 /db="GenBank"  
 /accession="AF010102"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_library="100 Plasmid Vector Library"  
 /vector="pUC19" (from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/)). The DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor oligonucleotides were used for a 5.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pmv2 (g1172114[gB]AI12072.1), a copy-number ligated with adaptor complementarity to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* (Stratagene) cells and plated on tetracycline resistance."

BASE COUNT  
 211 a 76 c 238 t

Query Match  
 Best Local Similarity 83.9% Pred. No. 7.7e+02;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 OR  
 1 ATATCGAATACCTGCTGATTTGATTTT 31  
 Db 558 AATGAGACCTGCTGATTTGATTTT 588

RESULT 10  
 B0002494 668 bp mRNA linear EST 26-MAR-2002  
 LOCUS B0002494.1 668 bp mRNA sequence.  
 DEFINITION B0002494.1 GI:19727394  
 VERSION B0002494.1 GI:19727394  
 KEYWORDS  
 EST, sapiens (human)  
 Homo sapiens  
 Butayocis; Metaco; Chorodai; Craniata; Vertebrata; Euteleostomi;  
 Mamalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.  
 Nucleotide sequence data from:  
 NC-CDS http://www.ncbi.nlm.nih.gov/nc-cds/  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 Submitted to GenBank  
 JOURNAL  
 COMMENT  
 Email: genbank@ncbi.nlm.nih.gov  
 Tissue Procurement: Dr. Jose Mercanade  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA sequencing by: Dr. M. Bento Soares, University of Iowa  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 Tissue Procurement: Dr. Jose Mercanade  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

FEATURES  
 source

Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /strain="CEB76/67"  
 /db="GenBank"  
 /accession="AF010102"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_library="100 Plasmid Vector Library"  
 /vector="pUC19" (from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/)). The DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor oligonucleotides were used for a 5.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pmv2 (g1172114[gB]AI12072.1), a copy-number ligated with adaptor complementarity to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* (Stratagene) cells and plated on tetracycline resistance."

BASE COUNT  
 234 a 96 c 114 g 223 t

Query Match  
 Best Local Similarity 74.2% Score 23; DB 12; Length 668;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 OR  
 1 ATATCGAATACCTGCTGATTTGATTTT 31  
 Db 150 AATGAGACCTGCTGATTTGATTTT 180

RESULT 11  
 C120192 814 bp DNA linear GSS 16-APR-2003  
 LOCUS C120192.1 814 bp DNA sequence.  
 DEFINITION C120192.1 GI:29899247  
 VERSION C120192.1 GI:29899247  
 KEYWORDS  
 EST, sapiens (human)  
 Homo sapiens  
 Butayocis; Metaco; Chorodai; Craniata; Vertebrata; Euteleostomi;  
 Mamalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.  
 Nucleotide sequence data from:  
 NC-CDS http://www.ncbi.nlm.nih.gov/nc-cds/  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 Submitted to GenBank  
 JOURNAL  
 COMMENT  
 Email: genbank@ncbi.nlm.nih.gov  
 Tissue Procurement: Dr. Jose Mercanade  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

FEATURES  
 source

Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /strain="CEB76/67"  
 /db="GenBank"  
 /accession="AF010102"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_library="100 Plasmid Vector Library"  
 /vector="pUC19" (from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/)). The DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor oligonucleotides were used for a 5.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pmv2 (g1172114[gB]AI12072.1), a copy-number ligated with adaptor complementarity to the insert adaptor and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* (Stratagene) cells and plated on tetracycline resistance."



/mol\_type="genomic DNA"  
 /strain="Liverpool"  
 /clone="NDL-5159"  
 /clone="NDL-5159"  
 /note="Vector: pSBEK1, Site 1: Hind III. The library was  
 by David Severn at the University of Notre Dame and  
 Hongbin Zhang"

BASE COUNT 236 a 210 c 149 g 219 t  
 ORIGIN  
 Query Match 74.2%; Score 23; DB 29; Length 814;  
 Best Local Similarity 83.9%; Pred. No. 8.1e+02;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Or 1 ATGTGAACTGTGATTTGAAATTT 31  
 172 ATGTGAACTGTGATTTGAAATTT 142

RESULT 12  
 BB685747 232 bp mRNA linear EST 09-MAR-2002  
 LOCUS BB685747.1 GI:19264491  
 DEFINITION BB685747.1 GI:19264491  
 ACCESSION BB685747.1 GI:19264491  
 VERSION BB685747.1  
 SOURCE  
 ORGANISM  
 Glycine max (soybean)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;  
 rosids  
 Fabales; Fabaceae; Papilionales; Phaseolaceae;  
 Glycine

REFERENCE  
 1 (bases 1 to 232)  
 Shoemaker R., Karm P., Vothli L., Espalding T., Corry J. V., Zhang  
 W., Hill C., Bowers J., Peterson B., Swaller T., Gibbons W., Pege D., Harvey M., Schurk  
 W., Ratter E., Korn S., Shan T., Jackson Y., Cardenas M., McMan  
 Public Soybean EST Project  
 JOURNAL  
 Unpublished  
 COMMENT  
 Contact: Shoemaker R./Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1800  
 Email: rshoemaker@wustl.edu

FEATURES  
 source  
 1..434  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1063-4506"  
 /strain="Liverpool"  
 /tissue="germinating shoot, 24 hour germination"  
 /db\_xref="taxon:3847"  
 /note="Vector: pSBEK1, Site 1: Hind III. The library was  
 by David Severn at the University of Notre Dame and  
 Hongbin Zhang"

BASE COUNT 236 a 210 c 149 g 219 t  
 ORIGIN  
 Query Match 74.2%; Score 23; DB 29; Length 814;  
 Best Local Similarity 83.9%; Pred. No. 8.1e+02;  
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Or 1 ATGTGAACTGTGATTTGAAATTT 31  
 172 ATGTGAACTGTGATTTGAAATTT 142

poly(GT) sequence with a XhoI restriction site. EcoRI  
 adapters were ligated to the blunt-ended cDNA fragments  
 directionally cloned into the EcoRI-XhoI restriction site  
 of the pSBEK1 vector. The ligated cDNA fragments were  
 transformed into DH10B host cells (Gibco BRL). This  
 library was stored at -80°C in the presence of 15% glycerol  
 at the University of Iowa State University."

BASE COUNT 106 a 210 c 149 g 219 t  
 ORIGIN  
 Query Match 72.9%; Score 22.6; DB 12; Length 232;  
 Best Local Similarity 86.2%; Pred. No. 8.7e+02;  
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Or 2 TGTGAACTGTGATTTGAAATTT 30  
 74 TGTGAACTGTGATTTGAAATTT 102

RESULT 13  
 BB330627 434 bp mRNA linear EST 04-DEC-2001  
 LOCUS BB330627.1 GI:19264491  
 DEFINITION BB330627.1 GI:19264491  
 ACCESSION BB330627.1 GI:19264491  
 VERSION BB330627.1  
 SOURCE  
 ORGANISM  
 Glycine max (soybean)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;  
 rosids  
 Fabales; Fabaceae; Papilionales; Phaseolaceae;  
 Glycine

REFERENCE  
 1 (bases 1 to 434)  
 Shoemaker R., Karm P., Vothli L., Espalding T., Corry J. V., Zhang  
 W., Hill C., Bowers J., Peterson B., Swaller T., Gibbons W., Pege D., Harvey M., Schurk  
 W., Ratter E., Korn S., Shan T., Jackson Y., Cardenas M., McMan  
 Public Soybean EST Project  
 JOURNAL  
 Unpublished  
 COMMENT  
 Contact: Shoemaker R./Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1800  
 Email: rshoemaker@wustl.edu

FEATURES  
 source  
 1..434  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1040-2149"  
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 /tissue="germinating shoot, 24 hour germination"  
 /db\_xref="taxon:3847"  
 /note="Vector: pSBEK1, Site 1: Hind III. The library was  
 by David Severn at the University of Notre Dame and  
 Hongbin Zhang"

BASE COUNT 106 a 210 c 149 g 219 t  
 ORIGIN  
 Query Match 72.9%; Score 22.6; DB 12; Length 232;  
 Best Local Similarity 86.2%; Pred. No. 8.7e+02;  
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Or 2 TGTGAACTGTGATTTGAAATTT 30  
 74 TGTGAACTGTGATTTGAAATTT 102







|            |   |
|------------|---|
| PT         | new isolated <i>Enterococcus faecalis</i> polynucleotides and polypeptides            |
| PT         | - used to develop products for the detection of <i>Enterococcus</i> and for           |
| PT         | use in methods for prevention or attenuation of <i>Enterococcus</i>                   |
| PT         | infection.  |
| PT         | Claim 1, Page 429-438, 1064pp. English.   |
| BS         |   |
| CC         | A computer readable medium has been developed which has recorded on it                |
| CC         | 982 nucleotide sequences isolated from the <i>Enterococcus faecalis</i> genome.       |
| CC         | AA11233 to AA11919 represent these nucleotide sequences which are said                |
| CC         | primary nucleotide sequence of the <i>Enterococcus faecalis</i> genome with           |
| CC         | commercial importance. This products can be used to detect the presence               |
| CC         | of <i>Enterococcus faecalis</i> in samples. They can also be used for                 |
| CC         | diagnosing <i>Enterococcus</i> infection in an animal and which can be used to        |
| CC         | modulate the growth or pathogenicity of <i>Enterococcus faecalis</i> , or             |
| CC         | another related organism, in vivo or in vitro. In particular the                      |
| CC         | polypeptides encoded by the <i>Enterococcus faecalis</i> nucleotide sequences         |
| CC         | recorded in the medium can be used to prevent or attenuate an <i>Enterococcus</i>     |
| CC         | infection.  |
| SQ         | Sequence 17087 BP; 4734 A; 3683 G; 3245 G; 5415 T; 10 other;                          |
| Q          |   |
| Q          | Query Match   |
| Q          | Best Local Similarity 88.9%; Pred. No. 26;  |
| Q          | Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0                            |
| Q          |   |
| Q          | 4 TGAAGATGCTCAAAATATGCTGAC 30   |
| DB         | 11327 TGAAGATGCTCAAAATATGCTGAC 11301  |
| DB         |   |
| RESULT 5   |   |
| AS898779/c |   |
| ID         | AS898779 standard; DNA; 17087 BP.   |
| XX         |   |
| XX         | AS898779;   |
| XX         |   |
| XX         | 18-DEC-2002 (file entry)  |
| DT         |   |
| DT         | <i>Enterococcus faecalis</i> contig sequence #47.                                     |
| XX         |   |
| XX         | Computer readable medium; <i>Enterococcus faecalis</i> ; <i>alcalybe</i> ; growth     |
| XX         | pathogenicity; nucleic acid sequencing; fermenting sugar source; metabolite; vaccine; |
| XX         | biotech technology; antibacterial; modulator of nucleic acid expression;              |
| XX         | contigs; da.  |
| XX         |   |
| XX         | <i>Enterococcus faecalis</i> .  |
| XX         |   |
| XX         | US200120101c-NL.  |
| XX         |   |
| XX         | 29-MAR-2002.  |
| XX         |   |
| XX         | 04-MAY-1998; 98US-0070927.  |
| XX         |   |
| XX         | 04-MAY-1998; 98US-0070927.  |
| XX         |   |
| XX         | (KRON) KRONSC C A.  |
| XX         | (DILL) DILLON P J.  |
| XX         | (BARN) BARNES S U.  |
| XX         |   |
| XX         | Kunsch Ch, Dillon PJ, Barash S;   |
| XX         |   |
| XX         | WFI; 2002-750065/81.  |
| XX         |   |
| XX         | Computer readable medium having recorded on it a <i>Enterococcus faecalis</i>         |
| XX         | nucleotide sequence useful for detecting diseases related to                          |
| XX         | <i>Enterococcus</i> infection in animals  |
| XX         |   |
| XX         | Claim 1; Page -; 1199P. English.  |









QY 3 ATTAGAGCCGAGAGAAATGACTGAC 30  
 |||||  
 DB 1112 ATTAGAGCCGAGAGAAATGACTGAC 1139

RESULT 11  
 AB17238 1  
 AB17238 standard; DN, 508 BP.  
 AC AB17238;  
 XX 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster genomic polymolecule SEQ ID NO 3187.  
 XX  
 XX Protophila [Amelastat] biology; cell signalling; insecticide,  
 XX pharmaceutical; gene; ds.  
 XX  
 XX Drosophila melanogaster.  
 XX  
 XX M020017042-42.  
 XX  
 XX 27-SEP-2001.  
 XX  
 XX 23-MAR-2001, 2001NO-US029231.  
 XX  
 XX 23-MAR-2000; 2000US-1916379.  
 XX  
 XX 11-JUL-2000; 2000US-0614150.  
 XX  
 XX (PENE) PE CORP NY.  
 XX  
 XX Venter JC, Adams M, Li PMD, Wozniak EM,  
 XX WRI, 2001-656960/75.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX interactions -  
 XX  
 XX Claim 1, SEQ ID NO 3187; 21DP + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent.  
 XX The invention relates to a method for detecting 1000 or more genes  
 XX useful in developmental biology and in elucidating cell signalling and  
 XX cell-cell interactions in higher eukaryotes for the development of  
 XX insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX discloses genes and proteins from Drosophila melanogaster expressed DNA  
 XX (AB857737-AB872072).  
 XX The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format directly from WIGO  
 XX at ftp://ftp.int/pub/published\_pcr\_sequences.

XX Sequence 5088 BP; 1622 A; 1000 C; 938 G; 1528 T; 0 other;  
 XX  
 XX Query Match 66.7%; Score 20; DB 23; Length 5088;  
 XX Best Local Similarity 82.1%; Pred. No. 1.7e+02;  
 XX Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATTAGAGCCGAGAGAAATGACTGAC 28  
 |||||  
 DB 2570 ATTAGAGCCGAGAGAAATGACTGAC 2597

RESULT 12  
 AB890521/c  
 ID AB890521 standard; DN, 2365589 BP.  
 XX  
 XX AB890521;  
 XX  
 XX 16-MAY-2002 (first entry)  
 XX  
 XX Genomic sequence of Lactococcus lactis IL1403.

XX  
 XX Bioprinting; biodegradation; lactic bacterium; yogurt; cheese; ds.  
 XX  
 XX Lactococcus lactis IL1403.  
 XX  
 XX FR2807446-A1.  
 XX  
 XX 12-OCT-2001.  
 XX  
 XX 11-APR-2000; 2000FR-0004630.  
 XX  
 XX 11-APR-2000; 2000FR-0004630.  
 XX  
 XX (INR) INRA INST NAT RECH AGRICOMTOPE.  
 XX  
 XX Bolotche A, Scrobin A, Romani P, Ehrlich SD;  
 XX WPI, 2002-043418/06.  
 XX  
 XX New nucleotide sequence useful in the identification of Lactococcus  
 XX lactis and related species -  
 XX  
 XX Claim 1; SEQ ID 1; 2504bp; French.

XX The present invention is related to a Lactococcus lactis nucleotide  
 XX sequence (AB890521) and related proteins (AB853300-AB855621). The  
 XX nucleic acid sequence is useful in the detection and/or amplification of  
 XX nucleic acid sequences, particularly those of the genus Lactococcus or  
 XX related species. The invention is useful for the detection of  
 XX bioprinting or biodegradation of a composition of interest. The  
 XX invention helps research in lactic bacteria, particularly useful in the  
 XX production of yogurt and cheese.  
 XX The present invention, patent is based on equivalent patent  
 XX M020017734 published 18-OCT-2001, which is available in electronic  
 XX format directly from WIGO at ftp://ftp.int/pub/published\_pcr\_sequences.

XX Sequence 2365589 BP; 765914 A; 415631 C; 420487 G; 763297 T; 0 other;  
 XX  
 XX Query Match 66.7%; Score 20; DB 24; Length 2365589;  
 XX Best Local Similarity 82.1%; Pred. No. 3.1e+02;  
 XX Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATTAGAGCCGAGAGAAATGACTGAC 28  
 |||||  
 DB 1391056 ATTAGAGCCGAGAGAAATGACTGAC 1391029

RESULT 13  
 AB872236/c  
 ID AB872236 standard; DN, 508 BP.  
 XX  
 XX AB872236;  
 XX  
 XX 19-SEP-2001 (first entry)  
 XX  
 XX Human cervical cancer marker nucleic acid 3510.  
 XX  
 XX Cervical cancer; cytotoxic; pre-malignant condition; gene therapy; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX M0200142467-A2.  
 XX  
 XX 14-JUN-2001.  
 XX  
 XX 08-DEC-2000; 2000NO-US33312.  
 XX  
 XX 08-DEC-1999; 99US-0169691.  
 XX  
 XX 21-DEC-1999; 99US-0113350.  
 XX  
 XX 14-MAR-2000; 2000US-0189315.  
 XX  
 XX 13-MAY-2000; 2000US-0203921.  
 XX  
 XX 21-JUL-2000; 2000US-0220134.

(MILL-) MILLERINUM PREDICTIVE MEDICINE INC.

Schlegel R, Deeds J, Berger A, Zhao X;

WPI: 2001-375066/39.

New isolated nucleic acid for diagnosing and treating cervical cancer -  
for assessing and detecting compounds for treating the cancer -  
Claim 1, Page 670, 105pp; English.

The invention relates to novel genes (AAH68727-AAH7383) associated with  
cervical cancer with cytoskeletal activity. The nucleic acids and encoded  
polypeptides are useful to assess the condition of a patient with  
cervical cancer or has a pre-malignant condition to monitor the  
progression of cervical cancer or a premalignant condition in a patient;  
and to select and/or assess the efficacy of a compound or therapy for  
inhibiting cervical cancer in a patient. The nucleic acids may also be  
useful for gene therapy.

Sequence 508 BP; 108 A; 143 C; 129 G; 128 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 508;  
Best Local Similarity 84.6%; Prod. No. 1.9e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
2 TTTAAAGCCGAGAAATCTGCTG 27  
Db 144 TTAGAGACCCAGAGATGACGCTG 119

RESULT 14  
AAH63370/C  
AAH63370 standard; cDNA; 539 BP.

AAH63370;

13-SEP-2001 (first entry)

Human cervical cancer marker nucleic acid 644.

Cervical cancer; cytoskeletal; pre-malignant condition; gene therapy; ss.

Homo sapiens.

W0200142467-A2.

14-JUN-2001.

06-DEC-2000; 2000NC-053312.

08-DEC-1999; 99US-0159481.

08-DEC-1999; 99US-0159481.

14-MAR-2000; 2000US-0189315.

12-MAY-2000; 2000US-0203291.

09-JUN-2000; 2000US-0210600.

21-JUN-2000; 2000US-0220114.

(MILL-) MILLERINUM PREDICTIVE MEDICINE INC.

Schlegel R, Deeds J, Berger A, Zhao X;

WPI: 2001-375066/39.

New isolated nucleic acid for diagnosing and treating cervical cancer -  
and for assessing and detecting compounds for treating the cancer -  
Claim 1, Page 215-216; 105pp; English.

The invention relates to novel genes (AAH68727-AAH7383) associated with  
cervical cancer with cytoskeletal activity. The nucleic acids and encoded  
polypeptides are useful to assess if a patient is afflicted with

CC cervical cancer or has a pre-malignant condition; to monitor the  
CC progression of cervical cancer in a patient;  
CC and to select and/or assess the efficacy of a compound or therapy for  
CC inhibiting cervical cancer in a patient. The nucleic acids may also be  
CC useful for gene therapy.

Sequence 539 BP; 118 A; 152 C; 137 G; 132 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 539;  
Best Local Similarity 84.6%; Prod. No. 1.9e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
2 TTTAAAGCCGAGAAATCTGCTG 27  
Db 152 TTAGAGACCCAGAGATGACGCTG 127

RESULT 15  
AAH7172/C  
AAH7172 standard; cDNA; 547 BP.

AAH7172;

13-SEP-2001 (first entry)

Human cervical cancer marker nucleic acid 2446.

Cervical cancer; cytoskeletal; pre-malignant condition; gene therapy; ss.

Homo sapiens.

W0200142467-A2.

14-JUN-2001.

06-DEC-2000; 2000NC-053312.

08-DEC-1999; 99US-0169481.

21-DEC-1999; 99US-0171350.

14-MAR-2000; 2000US-0189315.

09-JUN-2000; 2000US-0210600.

21-JUN-2000; 2000US-0220114.

(MILL-) MILLERINUM PREDICTIVE MEDICINE INC.

Schlegel R, Deeds J, Berger A, Zhao X;

WPI: 2001-375066/39.

New isolated nucleic acid for diagnosing and treating cervical cancer -  
and for assessing and detecting compounds for treating the cancer -  
Claim 1, Page 513, 105pp; English.

The invention relates to novel genes (AAH68727-AAH7383) associated with  
cervical cancer with cytoskeletal activity. The nucleic acids and encoded  
polypeptides are useful to assess the condition of a patient with  
cervical cancer or has a pre-malignant condition to monitor the  
progression of cervical cancer or a premalignant condition in a patient;  
and to select and/or assess the efficacy of a compound or therapy for  
inhibiting cervical cancer in a patient. The nucleic acids may also be  
useful for gene therapy.

Sequence 547 BP; 119 A; 153 C; 142 G; 133 T; 0 other;

Query Match 65.3%; Score 19.6; DB 22; Length 547;  
Best Local Similarity 84.6%; Prod. No. 1.9e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
2 TTTAAAGCCGAGAAATCTGCTG 27  
Db 161 TTAGAGACCCAGAGATGACGCTG 136

Search completed, December 18, 2003, 10:29:56  
SD Case : 203,721 recs

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GenScan version 5.1.6  
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ON nucleic - nucleic search, using sw model

Run on: December 18, 2003, 09:02:17 / Search time 43.7706 seconds

(without alignments) 302,521 Million cell updates/sec

Title: US-09-889-491-13

Sequence: 1 atctagagcccaagaacacgcgtac 30

Scoring table:

Gapco 10.0, Gapext 1.0

Searched:

569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Litering filter 45 summaries

Database:

- 1: /cgm2\_6/pdata2/lin/5A\_COXb.seq\*
- 2: /cgm2\_6/pdata2/lin/5B\_COXb.seq\*
- 3: /cgm2\_6/pdata2/lin/5B\_COXb.seq\*
- 4: /cgm2\_6/pdata2/lin/5B\_COXb.seq\*
- 5: /cgm2\_6/pdata2/lin/5B\_COXb.seq\*
- 6: /cgm2\_6/pdata2/lin/backfills.seq\*

Prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID              | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| c 1        | 19.4  | 64.7        | 6854   | US-08-468-036-4    | Sequence 4, App1   |
| c 2        | 19.4  | 64.7        | 6854   | US-08-468-036-4    | Sequence 4, App1   |
| c 3        | 19.2  | 64.0        | 2403   | US-08-441-139-17   | Sequence 38, App1  |
| c 4        | 19.2  | 64.0        | 2403   | US-08-441-139-17   | Sequence 38, App1  |
| c 5        | 19.2  | 64.0        | 2403   | US-08-441-139-17   | Sequence 38, App1  |
| c 6        | 19.2  | 64.0        | 2403   | US-08-441-139-17   | Sequence 38, App1  |
| c 7        | 18.4  | 61.3        | 429    | US-08-686-878A-6   | Sequence 8, App1   |
| c 8        | 18.4  | 61.3        | 429    | US-08-686-878A-6   | Sequence 8, App1   |
| c 9        | 18.4  | 61.3        | 429    | US-08-686-878A-6   | Sequence 8, App1   |
| c 10       | 18.4  | 61.3        | 429    | US-08-686-878A-6   | Sequence 8, App1   |
| c 11       | 18    | 60.0        | 2179   | US-08-426-426A-1   | Sequence 19, App1  |
| c 12       | 18    | 60.0        | 2179   | US-08-426-426A-1   | Sequence 19, App1  |
| c 13       | 18    | 60.0        | 2179   | US-08-426-426A-1   | Sequence 19, App1  |
| c 14       | 18    | 60.0        | 2179   | US-08-426-426A-1   | Sequence 19, App1  |
| c 15       | 17.8  | 59.3        | 8398   | US-09-328-352-1022 | Sequence 5, App1   |
| c 16       | 17.8  | 59.3        | 8398   | US-09-328-352-1022 | Sequence 5, App1   |
| c 17       | 17.8  | 59.3        | 8398   | US-09-328-352-1022 | Sequence 5, App1   |
| c 18       | 17.8  | 59.3        | 8398   | US-09-328-352-1022 | Sequence 5, App1   |
| c 19       | 17.6  | 58.7        | 4749   | US-09-613-034-189  | Sequence 189, App1 |
| c 20       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |
| c 21       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |
| c 22       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |
| c 23       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |
| c 24       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |
| c 25       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |
| c 26       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |
| c 27       | 17.4  | 58.0        | 741    | US-09-613-034-189  | Sequence 189, App1 |

|      |      |      |      |   |                 |                  |
|------|------|------|------|---|-----------------|------------------|
| 28   | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 29 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 30 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 31 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 32 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 33 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 34 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 35 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 36 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 37 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 38 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 39 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 40 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 41 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 42 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 43 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 44 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |
| c 45 | 17.2 | 57.3 | 1082 | 1 | US-08-716-301-5 | Sequence 5, App1 |

# ALIGNMENTS

|   |   |
|---|---|
| US-08-468-036-4/c   | US-08-468-036-4/c   |
| Sequence 4, Applicant US/08468036                                   | Sequence 4, Applicant US/08468036                                   |
| Patent No. 5728906  | Patent No. 5728906  |
| GENERAL INFORMATION:  | GENERAL INFORMATION:  |
| APPLICANT: Hockley, Anthony J.                                      | APPLICANT: Hockley, Anthony J.                                      |
| TITLE OF INVENTION: Materials and Methods Relating to Proteins that | TITLE OF INVENTION: Materials and Methods Relating to Proteins that |
| INTERACT WITH CASEIN KINASE I                                       | INTERACT WITH CASEIN KINASE I                                       |
| CORRESPONDENCE ADDRESS:   | CORRESPONDENCE ADDRESS:   |
| ADDRESS: Marshall, O'Toole, Gerstein, Murray & Porun                | ADDRESS: Marshall, O'Toole, Gerstein, Murray & Porun                |
| STREET: 6300 Sears Tower, 233 South Wacker Drive                    | STREET: 6300 Sears Tower, 233 South Wacker Drive                    |
| CITY: Chicago   | CITY: Chicago   |
| STATE: Illinois   | STATE: Illinois   |
| COUNTRY: United States of America                                   | COUNTRY: United States of America                                   |
| ZIP: 60606-6402   | ZIP: 60606-6402   |
| COMPUTER READABLE FORM:   | COMPUTER READABLE FORM:   |
| COMPUTER: IBM PC Compatible   | COMPUTER: IBM PC Compatible   |
| OPERATING SYSTEM: PC-DOS/MS-DOS                                     | OPERATING SYSTEM: PC-DOS/MS-DOS                                     |
| SOFTWARE: PatentIn Release #1.0, Version #1.25                      | SOFTWARE: PatentIn Release #1.0, Version #1.25                      |
| CURRENT APPLICATION DATA:   | CURRENT APPLICATION DATA:   |
| FILE NO. 06-JUN-1995  | FILE NO. 06-JUN-1995  |
| CLASSIFICATION: E30   | CLASSIFICATION: E30   |
| PRIOR APPLICATION: US 08/184,605                                    | PRIOR APPLICATION: US 08/184,605                                    |
| FILING DATE: 21-JAN-1994  | FILING DATE: 21-JAN-1994  |
| ATTORNEY/AGENT INFORMATION:   | ATTORNEY/AGENT INFORMATION:   |
| NAME: Mr. 5728906and, Greta E.                                      | NAME: Mr. 5728906and, Greta E.                                      |
| REGISTERED/UNREGISTERED: 5728906/11784                              | REGISTERED/UNREGISTERED: 5728906/11784                              |
| TELEPHONE/CALL INFORMATION:   | TELEPHONE/CALL INFORMATION:   |
| TELEPHONE: 312/474-6300   | TELEPHONE: 312/474-6300   |
| TELEFAX: 312/474-0448   | TELEFAX: 312/474-0448   |
| INFORMATION FOR SEQ ID NO: 4:                                       | INFORMATION FOR SEQ ID NO: 4:                                       |
| SEQUENCE CHARACTERISTICS:   | SEQUENCE CHARACTERISTICS:   |
| LENGTH: 6954 base pairs   | LENGTH: 6954 base pairs   |
| STRANDS: single   | STRANDS: single   |
| TOPOLOGY: linear  | TOPOLOGY: linear  |
| MOLECULE TYPE: DNA (genomic)  | MOLECULE TYPE: DNA (genomic)  |
| FEATURES:   | FEATURES:   |
| FEATURE: CDS  | FEATURE: CDS  |
| LOCATION: 2050..4053  | LOCATION: 2050..4053  |
| US-08-468-036-4   | US-08-468-036-4   |
| Query Match   | 64.7%, Score 13.4, DB 1, Length 6854,                               |

Best Local Similarity 79.3%; Pred. No. 38;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATAGAGCCCGAAGAAATCACTGAC 29

DB 2644 AATAGAGCCCGAAGAAATCACTGAC 2616

## RESULT 2

US-08-376-843-4/c

Sequence 4; Application US/0837643

GENERAL INFORMATION:

APPLICANT: DeMaegio, Anthony J.

ADDRESSES: Rockefeller, Neil F. and Methods Relating to Proteins

TITLE OF INVENTION: that interact with Casein Kinase I

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESSES: O'Toole, Geraldine, Murray & Borum

STREET: 3300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/376,843

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/184,605

FILING DATE: 21-JAN-1994

NAME: NO. 584674and, Greeta B.

REGISTRATION NUMBER: 35,102

TELEPHONE: 312/474-0448

TELEFAX: 312/474-0448

INVENTION ID NO.: 41

SEQUENCE CHARACTERISTICS:

LENGTH: 6854 base pairs

TYPE: nucleic acid

STRANDNESS: single

MODALITY: linear

MOLECULE TYPE: DNA (genomic)

NAME/KEY: CDS

SEQUENCE: 4

US-08-376-843-4

Query Match Similarity 64.7%; Score 19.4; DB 2; Length 6854;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATAGAGCCCGAAGAAATCACTGAC 29

DB 2644 AATAGAGCCCGAAGAAATCACTGAC 2616

## RESULT 3

Sequence 17; Application US/08441139

Patent No. 5779245

GENERAL INFORMATION:

ADDRESSES: O'Toole, Geraldine, Murray & Borum

TITLE OF INVENTION: that interact with Casein Kinase I

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESSES: O'Toole, Geraldine, Murray & Borum

STREET: 3300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,139

FILING DATE: 06-JUN-1995

NAME/KEY: CDS

SEQUENCE: 4

US-08-441-139-17

Query Match Similarity 64.0%; Score 19.2; DB 1; Length 2403;  
Matches 21; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 AATAGAGCCCGAAGAAATCACTGAC 38

DB 1929 AATAGAGCCCGAAGAAATCACTGAC 1992

Query Match Similarity 64.0%; Score 19.2; DB 1; Length 2403;  
Matches 21; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATAGAGCCCGAAGAAATCACTGAC 29

DB 2644 AATAGAGCCCGAAGAAATCACTGAC 2616

Query Match Similarity 64.0%; Score 19.2; DB 1; Length 2403;  
Matches 21; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATAGAGCCCGAAGAAATCACTGAC 29

DB 2644 AATAGAGCCCGAAGAAATCACTGAC 2616

Query Match Similarity 64.0%; Score 19.2; DB 1; Length 2403;  
Matches 21; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATAGAGCCCGAAGAAATCACTGAC 29

DB 2644 AATAGAGCCCGAAGAAATCACTGAC 2616

Query Match Similarity 64.0%; Score 19.2; DB 1; Length 2403;  
Matches 21; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATAGAGCCCGAAGAAATCACTGAC 29

DB 2644 AATAGAGCCCGAAGAAATCACTGAC 2616

CLASSIFICATION: 530  
 PRIORITY: 38/US 08/184,605  
 APPLICATION NUMBER: 08/184,605  
 FILING DATE: 21-JUN-1994  
 ATTORNEY/AGENT INFORMATION: Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/31784  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3466 bp  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-469-935-38  
 Query Match 64.0%; Score 19.2; DB 1; Length 3466;  
 Best Local Similarity 87.5%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 ATATGAGACCCGAGAAATATGAC 24  
 Db 353 ATGAGACCCGAGAAATATGAC 330  
 RESULT 5  
 US-08-376-843-38/C  
 Sequence 4, Application US/08376843  
 Patent No. 5846764  
 GENERAL INFORMATION:  
 APPLICANT: DeGaglio, Anthony J.  
 ATTORNEY/AGENT INFORMATION: Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/31784  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3466 bp  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-469-935-38  
 Query Match 64.0%; Score 19.2; DB 1; Length 3466;  
 Best Local Similarity 87.5%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 ATATGAGACCCGAGAAATATGAC 24  
 Db 353 ATGAGACCCGAGAAATATGAC 330  
 RESULT 5  
 US-08-376-843-38/C  
 Sequence 4, Application US/08376843  
 Patent No. 5846764  
 GENERAL INFORMATION:  
 APPLICANT: DeGaglio, Anthony J.  
 ATTORNEY/AGENT INFORMATION: Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/31784  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3466 bp  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-469-935-38  
 Query Match 64.0%; Score 19.2; DB 1; Length 3466;  
 Best Local Similarity 87.5%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 ATATGAGACCCGAGAAATATGAC 24  
 Db 353 ATGAGACCCGAGAAATATGAC 330

MOLECULE TYPE: DNA (genomic)  
 US-08-376-843-38  
 Query Match 64.0%; Score 19.2; DB 2; Length 3466;  
 Best Local Similarity 87.5%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 ATATGAGACCCGAGAAATATGAC 24  
 Db 353 ATGAGACCCGAGAAATATGAC 330  
 RESULT 6  
 US-08-728-956-2  
 Sequence 4, Application US/08728956  
 Patent No. 5708157  
 GENERAL INFORMATION:  
 APPLICANT: Hodges, Thomas K.  
 ATTORNEY/AGENT INFORMATION: Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/31784  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3466 bp  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-728-956-2  
 Query Match 63.3%; Score 19; DB 1; Length 613;  
 Best Local Similarity 81.5%; Pred. No. 37;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Oy 4 TGAACCCGAGAAATATGAC 30  
 Db 292 TGAACCCGAGAAATATGAC 318  
 RESULT 7  
 US-08-679-874-9/C  
 Sequence 4, Application US/0868679A  
 Patent No. 5708157  
 GENERAL INFORMATION:  
 APPLICANT: Jackson, Kenneth  
 ATTORNEY/AGENT INFORMATION: Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 27866/31784  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3466 bp  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-679-874-9/C  
 Query Match 63.3%; Score 19; DB 1; Length 613;  
 Best Local Similarity 81.5%; Pred. No. 37;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Oy 4 TGAACCCGAGAAATATGAC 30  
 Db 292 TGAACCCGAGAAATATGAC 318



```

1 TELX:
2 INFORMATION FOR SEQ ID NO: 189:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 1355 base pairs
5 TYPE: nucleic acid
6 STRANDEDNESS: single
7 TOPOLOGY: linear
8 MOLECULE TYPE: Genomic DNA
9
10 US-08-336-165A-189

```

|                       |              |              |              |             |
|-----------------------|--------------|--------------|--------------|-------------|
| Query Match           | 61.3%        | Score 18.4   | DB 4         | Length 1355 |
| Best Local Similarity | 75.3%        | Pred. No. 75 |              |             |
| Matches 22            | Conservative | 0            | Mismatches 7 | Indels 0    |
|                       |              |              | Gaps         | 0           |

|    |     |                             |      |
|----|-----|-----------------------------|------|
| Qy | 1   | ATATAGAGCCCAAGAAAATCAGCTGAC | 29   |
|    |     |                             |      |
| Db | 972 | ACACAGAAGCTGCGAAAGTCAGCTGAC | 1000 |

RESULT 10  
 US-09-734-674-3 / C  
 Patent No. 6398022  
 GENERAL INFORMATION:  
 APPLICANT: WEI, WING-HAI et al  
 TITLE OF INVENTION: HUMAN TRANSPORTER PROTEIN  
 TITLE OF INVENTION: IONIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS  
 FILE REFERENCE: CLO01018  
 CURRENT APPLICATION NUMBER: US/09/734,674  
 CURRENT PRIORITY DATE: 2009-12-15  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 3  
 TYPE: CDS  
 LENGTH: 202001  
 ORGANISM: human  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1..202001  
 OTHER INFORMATION: n="A", n="C or G"  
 US-09-734-674-3

|                          |        |                    |           |                |
|--------------------------|--------|--------------------|-----------|----------------|
| Query Match              | 61.3%; | Score 18.4;        | DB 4;     | Length 202001; |
| Best Local Similarity    | 78.6%; | Pred. NO. 1.6e+02; |           |                |
| Matches 22; Conservative | 0;     | Mismatches 6;      | Indels 0; |                |

```

Oy      1 ATATGAGGCCCMAGAAATCAGCTGA 28
          |||||  |  |  |  |  |  |  |
Db      170709 ATATGAGGTCMAATGAACTCAGTTGA 170682

```

US-08-558-111A-37  
 RESULT 11  
 Patent No. 6348138  
 GENERAL INFORMATION:  
 APPLICANT: Black, Michael  
 APPLICANT: Kowles, David  
 APPLICANT: Nichols, Robert  
 APPLICANT: Stodola, Richard  
 NUMBER OF SEQUENCES: 512  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Beckman Research Corporation  
 ADDRESS: 10000 Wilshire Road  
 CITY: Culver City, CA 90230  
 STATE: CA  
 COUNTRY: USA  
 COMPUTER: 64019  
 COMPUTER READING ROOM:  
 MEDICAL TYPE: Diabetic

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0.C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A

```

```

; INFORMATION FOR SEQID NO: 37
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 2179 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
US-08-858-207A-37

```

|                          |        |                   |           |              |
|--------------------------|--------|-------------------|-----------|--------------|
| Query Match              | 60.0%; | Score 18;         | DB 4;     | Length 2179; |
| Best Local Similarity    | 80.8%; | Prd. No. 1.2e+02; |           |              |
| Matches 21; Conservative | 0;     | Mismatches 5;     | Indels 0; | Gaps 0       |

Oy 3 ATAGAGCCCAAGAAAAATCAGCTGA 28  
 Db 803 ATAGTAGCCTATGAAGATCAGCTAA 828

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COMPIER FEATURES: POWER: 5.25 inch, 360 kb storage  
COMPIER: INTEL 8086  
OPERATING SYSTEM: PC/MS-DOS  
SOFTWARE: wordperfect  
CURRENT ACCOUNT NUMBER: 13911004  
DATE: 07/792, 865D  
FILING DATE: 13911004  
CLASSIFICATION: 435  
EXPLANATION: DATA  
FILED: 07/1990  
FILING DATE: April 3, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: MICHON, ALVIN  
REFERENCE/DOCKET NUMBER: 4,354  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (412) 522-7100  
TELETYPE: (412) 522-7200  
INFORMATION FOR SSO ID NO.: 1  
SEQUENCE CHARACTERISTICS:





```

Patent No. 6528260
GENERAL INFORMATION:
INVENTOR: Boudreau, et al, Marta
APPLICANT: Chumakov, Ilya
INVENTOR ADDRESS: 1800 Avenue du Parc, Montreal, Quebec, Canada
APPLICANT ADDRESS: 1800 Avenue du Parc, Montreal, Quebec, Canada
FILE REFERENCE: 62 US, CIP
CURRENT FILING DATE: 2000-09-22
CURRENT APPLICATION NUMBER: US/09/671,317
PRIORITY FILING DATE: 2000-09-22
PRIORITY APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US 60/131,961
NUMBER OF SEQ ID NOS: 977
SEQ ID NO: 87
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
NAME/KEY: allele
LOCATION: 497
OTHER INFORMATION: 12-662-80 : polymorphic base G or C
NAME/KEY: misc_binding
LOCATION: 472, 496
OTHER INFORMATION: 12-662-80.mis1, potential
NAME/KEY: misc_binding
LOCATION: 498, 517
OTHER INFORMATION: 12-662-80.mis2, potential complement
NAME/KEY: primer_bind
LOCATION: 418, 435
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 474, 100
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 485, 109
OTHER INFORMATION: 12-662-80 potential probe
NAME/KEY: misc_feature
LOCATION: 24,726,739
OTHER INFORMATION: n=a, 5', c or t
US-09-671-317-387
Query Match 59.3%; Score 17.8; DB 4; Length 1000;
Beat Local Similarity 75.9%; Evid No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATATGAGGCCAGAGAAATTCAGCTGAC 29
DB 977 ATGTGAGAGACACAGAAAAAGGCTTGAC 999

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Search completed: December 18, 2003, 09:04:15  
 Job time : 49.7705 secs



FEATURE:  
 NAME: CNE  
 LOCATION: 11... (12577)  
 US-09-815-242-4797

Query Match 74.0% Score 22.2 DB 9; Length 2577;  
 Best Local Similarity 84.9%  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TAGAGCCGAGAAAATGCGTACG 30

DB 1520 TAGAGCCGAGAAAATGCGTACG 1546

RESULT 2

US-09-070-927A-47/c

Sequence 47; Application US/09070927A

Patent No. US20020120115A1

INVENTOR: Steven A. Kunsch

APPLICANT: Patrick J. Dillon

ATTORNEY: Steven A. Kunsch

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

INVENTION NO. 1520

CORRESPONDENCE ADDRESS:

ADDRESSER: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION NUMBER: US/09/070,927A

FILING DATE: 04-May-2000

CLASSIFICATION: -UNKNOWN-

PRIOR APPLICATION NUMBER: 60/046,655

FILING DATE: 1997-05-16

APPLICATION NUMBER: 60/044,031

APPLICATION NUMBER: 60/066,009

FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:

NAME: KUNTSCH, R. HOOVER

ADDRESS: 1520

REFERENCE/DOCID NUMBER: P3369

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 308-8504

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 17087 base pairs

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-070-927A-47

Query Match 74.0% Score 22.2 DB 10; Length 17087;  
 Best Local Similarity 86.9%  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TAGAGCCGAGAAAATGCGTACG 30

DB 11327 TAGAGCCGAGAAAATGCGTACG 11301

RESULT 3

US-10-027-632-285052/c

Sequence 285052; Application US/10027632

Patent No. US20020040725B

INVENTOR: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-09-09

SOFTWARE: Painted for Windows Version 4.0

SEQ ID NO 285052

LENGTH: 1923

ORGANISM: Human

US-10-027-632-285052

Query Match 88.0% Score 20.4; DB 13; Length 1923;  
 Best Local Similarity 86.0%  
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGATGCGAGAAAATGCGTACG 30

DB 1916 AATATGATGCGAGAAAATGCGTACG 1887

RESULT 4

US-10-027-632-285052/c

Sequence 285052; Application US/10027632

Patent No. US20020040725B

INVENTOR: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: Painted for Windows Version 4.0

SEQ ID NO 285052

LENGTH: 1923

ORGANISM: Human

US-10-027-632-285052

Thu Dec 18 13:30:46 2003

Query Match 66.0%; Score 20.4; DB 14; Length 1933;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ATTTAGAGCCCAAGAAAATTCAGCTGACC 30  
 DB 1316 ATTTAGAGCCCAAGAAAATTCAGCTGACC 1887

RESULT 5  
 US-09-880-107-2406  
 / Sequence 2406; Application US/09880107  
 / Patent No. US20020142981A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Genentech, Inc.  
 / APPLICANT: Vockley, Joseph G.  
 / APPLICANT: Scheif, Dwe  
 / APPLICANT: Gene Logic, Inc.  
 / TITLE OF INVENTION: Gene expression profiles in liver cancer  
 / FILE REFERENCE: 44921-5028-00  
 / CURRENT APPLICATION NUMBER: US/09/880,107  
 / CURRENT FILING DATE: 2001-06-14  
 / PRIOR APPLICATION NUMBER: US 60/211,379  
 / PRIOR FILING DATE: 2000-06-08  
 / PRIOR APPLICATION NUMBER: US 60/237,054  
 / PRIOR FILING DATE: 2000-10-02  
 / NUMBER OF SEQ ID NOS: 3950  
 / SOFTWARE: GENES REG. BY MYCN ACTIVATION  
 / SEQ ID NO 2406  
 / LENGTH: 3610  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / OTHER INFORMATION: Genbank Accession No. US20020142981A1 M63216  
 US-09-880-107-2406

Query Match 66.7%; Score 20; DB 10; Length 3610;  
 Best Local Similarity 82.1%; Pred. No. 2.2e+02;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 ATTTAGAGCCCAAGAAAATTCAGCTGACC 30  
 DB 1112 ATTTAGAGCCCAAGAAAATTCAGCTGACC 1139

RESULT 6  
 US-09-873-367C-721  
 / Sequence 721; Application US/09873367C  
 / Publication No. US20030165839A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Young, Paul  
 / APPLICANT: Sedgell, Daniel  
 / APPLICANT: Redress, Gregory  
 / APPLICANT: Genentech, Inc.  
 / APPLICANT: Rhee, Retaeh  
 / APPLICANT: Carter, Retaeh  
 / TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
 / FILE REFERENCE: 44921-5028-00  
 / CURRENT APPLICATION NUMBER: US/09/873,367C  
 / CURRENT FILING DATE: 2003-04-29  
 / PRIOR APPLICATION NUMBER: U.S. 60/236,891  
 / PRIOR FILING DATE: 2000-09-23  
 / PRIOR APPLICATION NUMBER: U.S. 60/236,842  
 / PRIOR FILING DATE: 2000-09-23  
 / PRIOR APPLICATION NUMBER: U.S. 60/244,867  
 / PRIOR FILING DATE: 2000-11-01  
 / PRIOR FILING DATE: 2000-11-01  
 / NUMBER OF SEQ ID NOS: 1067  
 / SOFTWARE: GENES REG. BY MYCN ACTIVATION  
 / SEQ ID NO 721  
 / LENGTH: 3610

QY TYR: DNA Homo sapiens  
 US-09-873-367C-721  
 / ORGANISM: Homo sapiens  
 / TYPE: DNA  
 / FEATURE:  
 / OTHER INFORMATION: Genbank Accession No. US20030165839A1 M63216

Query Match 66.7%; Score 20; DB 13; Length 3610;  
 Best Local Similarity 82.1%; Pred. No. 2.2e+02;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 ATTTAGAGCCCAAGAAAATTCAGCTGACC 30  
 DB 1112 ATTTAGAGCCCAAGAAAATTCAGCTGACC 1139

RESULT 7  
 US-10-084-817-30  
 / Sequence 30; Application US/10084817  
 / Publication No. US20030119009A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Susan Shattuck  
 / APPLICANT: Sharon M. Pilon  
 / APPLICANT: Sharon M. Pilon  
 / APPLICANT: Sharon M. Pilon  
 / TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
 / FILE REFERENCE: 44921-5028-00  
 / CURRENT APPLICATION NUMBER: US/10/084,817  
 / CURRENT FILING DATE: 2002-02-28  
 / PRIOR APPLICATION NUMBER: US 60/270,764  
 / PRIOR FILING DATE: 2002-02-28  
 / NUMBER OF SEQ ID NOS: 365  
 / SOFTWARE: PERL Program  
 / SEQ ID NO 30  
 / LENGTH: 3702  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / OTHER INFORMATION: Genbank Accession No. US20030119009A1 131235GB1  
 US-10-084-817-30

Query Match 66.7%; Score 20; DB 15; Length 3702;  
 Best Local Similarity 82.1%; Pred. No. 2.2e+02;  
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 ATTTAGAGCCCAAGAAAATTCAGCTGACC 30  
 DB 1328 ATTTAGAGCCCAAGAAAATTCAGCTGACC 1355

RESULT 8  
 US-09-918-995-36137  
 / Sequence 36137; Application US/09918995  
 / Publication No. US20030073823A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Hesp, Inc.  
 / APPLICANT: FROM VARIOUS CDNA LIBRARIES  
 / TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 / FILE REFERENCE: 20411-756  
 / CURRENT APPLICATION NUMBER: US/09/918,995  
 / CURRENT FILING DATE: 2003-01-20  
 / PRIOR APPLICATION NUMBER: US 60/236,076  
 / PRIOR FILING DATE: 1999-01-20  
 / NUMBER OF SEQ ID NOS: 38054  
 / SOFTWARE: FASTEST for Windows Version 3.0  
 / SEQ ID NO 36137  
 / LENGTH: 405  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / OTHER INFORMATION: Genbank Accession No. US20030073823A1 1355

Query Match 65.6%; Score 19.6; DB 11; Length 405;  
 Best Local Similarity 84.3%; Pred. No. 2.2e+02;  
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTTAAAGCCCAAAAATTCAGTGC 27  
DB 258 TTTAAAGCCCAAAAATTCAGTGC 253

RESULT 9  
US-09-742-311-3  
Sequence 3, Application US/09742311  
Patent No. US2002028773A1  
GENERAL INFORMATION:  
APPLICANT: Nant, David G.  
TITLE OF INVENTION: IDENTIFICATION AND MAPPING OF SINGLE NUCLEOTIDE  
POLYNUCLEOTIDES IN THE HUMAN GENOME  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
AND USES THEREOF  
CURRENT APPLICATION NUMBER: US/09/742,311  
CURRENT FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 4  
SEQ ID NO: FASTSEQ for Windows Version 4.0  
LENGTH: 52354  
TYPE: DNA  
ORGANISM: Human  
NAME/KEY: misc feature  
LOCATION: (1)... (52354)  
OTHER INFORMATION: n = A,T,C or G  
US-09-742-311-3  
Query Match 65.3%; Score 19.6; DB 9; Length 52354;  
Best Local Similarity 84.6%; Pred. No. 5.2e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3 ATTAAGCCCAAAAATTCAGTGC 28  
DB 30034 ACGAGCTGTCTATTAATAATTCAGTGC 30059

RESULT 10  
US-09-815-343-1379/C  
Sequence 1379, Application US/09815343  
Patent No. US2001005596A1  
GENERAL INFORMATION:  
APPLICANT: Mesinger, Madeline  
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
PREVENTION OF COLON CANCER  
TITLE REFERENCE: 2101.1.504  
CURRENT APPLICATION NUMBER: US/09/815,343  
CURRENT FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 1556  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 1379  
LENGTH: 406  
TYPE: DNA  
ORGANISM: Homo sapien  
NAME/KEY: misc feature  
LOCATION: (1)... (406)  
OTHER INFORMATION: n = A,T,C or G  
US-09-815-343-1379  
Query Match 64.7%; Score 19.4; DB 9; Length 406;  
Best Local Similarity 79.3%; Pred. No. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATTAAGCCCAAAAATTCAGTGC 29  
DB 154 AATTAAGCTGTCTATTAATAATTCAGTGC 126

RESULT 11

US-10-027-632-14709/C  
Sequence 14709, Application US/10027632  
Patent No. US2002024075A5  
GENERAL INFORMATION:  
APPLICANT: Nant, David G.  
TITLE OF INVENTION: IDENTIFICATION AND MAPPING OF SINGLE NUCLEOTIDE  
POLYNUCLEOTIDES IN THE HUMAN GENOME  
TITLE OF INVENTION: POLYNUCLEOTIDES IN THE HUMAN GENOME  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/198,483  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 14709  
LENGTH: 837  
TYPE: DNA  
ORGANISM: Human  
NAME/KEY: misc feature  
LOCATION: (1)... (837)  
OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-14709  
Query Match 64.0%; Score 19.2; DB 13; Length 837;  
Best Local Similarity 80.8%; Pred. No. 5.2e+02;  
Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 5 AAGAGCCCAAAAATTCAGTGC 30  
DB 80 AATTAAGCTGTCTATTAATAATTCAGTGC 55

RESULT 12  
US-10-027-632-14709/C  
Sequence 14709, Application US/10027632  
GENERAL INFORMATION:  
APPLICANT: Nant, David G.  
TITLE OF INVENTION: IDENTIFICATION AND MAPPING OF SINGLE NUCLEOTIDE  
POLYNUCLEOTIDES IN THE HUMAN GENOME  
TITLE OF INVENTION: POLYNUCLEOTIDES IN THE HUMAN GENOME  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/198,483  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 14709  
LENGTH: 837  
TYPE: DNA  
ORGANISM: Human  
NAME/KEY: misc feature  
LOCATION: (1)... (837)  
OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-14709



Query Match 64.0%; Score 19.2; DB 10; Length 20561;  
Best Local Similarity 87.5%; Pred. No. 6.4e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 6 GAGGCCAAGAAAAATCGCTGAC 29  
|||||  
DB 19006 GAGGCCAAGAAAAATCGCTGAC 18983  
|||||

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Search completed: December 18, 2003, 10:22:57  
Job time : 968.902 secs





## FEATURES

source

Location/Qualifiers

1. 1086 "Wesembryanthemum corymbellum"  
/mol\_type="mRNA"  
/db\_xref="taxon:1544"  
/db\_type="epidermal bladder cells"  
/clone="136-xx" weeks old  
/clone="136-xx" weeks old

## BASE COUNT

305 a 235 c 256 g 270 t  
/note="Vector: Bluescript SK+, Site 1: EcoRI, Site 2: XhoI  
Plants stressed 6 weeks in 500mM NaCl"

## QUERY

Query Match 73.3%; Score 22; DB 10; Length 1066;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy

1 ATATGAGACCCGAGAAATATACCTGACAC 30

Db

1071 ATAGAGAGATCCGAGGAGGACCTGACATGAC 1042

## RESULT 2

BM980025 454 bp mRNA linear EST 11-FEB-2002  
LOCUS 95202805.v1 952 - BM980025 from Walbot Lab (reduced rRNA) Zea  
ACCESSION BM980025  
VERSION 1  
KEYWORDS 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
EST 1864925.1 GI:1864925.1

## SOURCE

Zea mays

## REFERENCE

1. (bases 1 to 454)  
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Equisetum, Fossils; Poaceae;禾本科;  
clade; Panicoideae; Andropogoneae; Zea.

## TITLE

Malzeo ESTs from various cDNA libraries sequenced at Stanford

## JOURNAL

Unpublished

## COMMENT

Contact: Walbot, V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: val@leland.stanford.edu  
Plate: 952025 row: E column: 05.

## FEATURES

source

Location/Qualifiers

1. 454 "Zea mays"  
/mol\_type="mRNA"  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

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library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

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library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
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oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

/clone\_116-952 - BM980025 from Walbot Lab (reduced rRNA  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

## BASE COUNT

119 a 130 c 99 g 106 t

## ORIGIN

119 a 130 c 99 g 106 t

## Query Match

72.0%; Score 21.6; DB 15; Length 454;  
Best Local Similarity 85.7%; Pred. No. 8.6e+02;  
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 TATGAGACCCGAGAAATATACCTGACAC 29

161 TATGAGAGATCCGAGGAGGACCTGACATGAC 188

## RESULT 3

EC966188 477 bp mRNA linear EST 02-FEB-2001  
DEFINITION 100008604.x1 1000 - Unigene 1 from Male Genome Project Zea mays  
ACCESSION EC966188  
VERSION 1  
KEYWORDS 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
EST 12969244 GI:12969244

## SOURCE

Zea mays

## REFERENCE

1. (bases 1 to 477)  
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
clade; Panicoideae; Andropogoneae; Zea.

## AUTHORS

Walbot, V.

Unpublished

## TITLE

Malzeo ESTs from various cDNA libraries sequenced at Stanford

## JOURNAL

Unpublished

Contact: Walbot, V

## COMMENT

Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: val@leland.stanford.edu  
Plate: 100008 row: G column: 04.

## FEATURES

source

Location/Qualifiers

1. 477 "Zea mays"  
/mol\_type="mRNA"  
/note="Vector: pUC19; Site 1: EcoRI, Site 2: XhoI; The  
library was prepared by George Rudenko using poly (A)  
selected RNA and universal Ribosome cDNA Synthesis System  
oligo(dT) primers in separate reactions and amplified with  
EcoRI adapters. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-differentially cloned  
chemically into pUC19 vector. Blue-white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

## BASE COUNT

116 a 143 c 113 g 105 t

## ORIGIN

116 a 143 c 113 g 105 t

Query Match 72.0%; Score 21.6; DB 10; Length 477;  
Best Local Similarity 85.7%; Pred. No. 8.7e+02;  
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 TATGAGACCCGAGAAATATACCTGACAC 29

102 TATGAGAGATCCGAGGAGGACCTGACATGAC 129

## RESULT 4

AT174933 552 bp mRNA linear EST 02-FEB-2000  
DEFINITION 60602406.x2 606 - Ear tissue cDNA library from Cornbelt lab Zea  
ACCESSION AT174933  
VERSION 1  
KEYWORDS 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
EST 15030739 GI:15030739

## SOURCE

Zea mays

## ORIGIN

Unpublished



Db 135 ATGTAAGCCGAGAAATGCACTGAC 108

RESULT 7  
LOCUS AT112254/c  
DEFINITION AT112254  
ACCESSION AT112254  
KEYWORDS AT112254.1 GI:21216844  
SOURCE HNC  
ORGANISM HNC  
Zea mays  
Bakayocet; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACIND  
1. 649 bp DNA linear HNC 17-OCT-2002

REFERENCE  
AUTHORS Halvey C.F., Dolan M., Mao G.H., Vogel J.M., Willett M.S., Arthur L.W., Hanley M., Morgante M., and Tingey S.V.  
TITLE Male Mapping Project/DuPont Consensus Sequences for Design of Unpublished (2002)  
JOURNAL (bases 1 to 649)  
REFERENCE Coe E.H.  
AUTHORS Subtilled (25-Apr-2003) Male Mapping Project, University of Missouri, Columbia, MO 65211, USA  
JOURNAL If you are interested in getting corresponding physical clones, these are publicly available from ZMBB and may be found by BLAST [www.igb.org](http://www.igb.org) or NCBI [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). When the source of the male DNA sequences is either Virginia Waldb. Stanford or Pat Schmale, Iowa State, then clones may be requested from ZMBB: [www.zmbb.org](http://www.zmbb.org)

FEATURES  
SOURCE 1..649  
Location/Qualifiers  
/organism="Zea mays"  
/db\_xref="taxon:633041"  
/db\_xref="taxon:4577"  
/clone\_id="Male Mapping Project/DuPont Consensus  
Library: This sequence is part of a project of EST assembly resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration with the Male Mapping Project.  
Bases 131 g 172 c 25 others

BASE COUNT 175 a 146 c 131 g 172 c 25 others

ORGANISM

Query Match 72.0% Score 21.6; DB 11; Length 649;  
Best Local Similarity 85.7% Pred. No. 9.2e+02;  
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATGTAAGCCGAGAAATGCACTGAC 30  
DB 615 ATGTAAGCCGAGAAATGCACTGAC 588

RESULT 8  
LOCUS CC304082/c  
DEFINITION CC304082.1 GM:30675523  
ACCESSION CC304082.1 GI:30675523  
KEYWORDS CC304082.1 GI:30675523  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus (chicken)  
Bakayocet; Aves; Neognathae; Galliformes; Phasianidae;  
1. 940 bp DNA linear GSS 13-MAY-2003

REFERENCE  
AUTHORS Rasmussen, J., Adams, M.D., Newman, W., Malek, J., de Jong, P., and Venter, J.C.

AUTHORS Krentler, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Matern, W., Graves, T., Madis, E., and Wilson, R.  
TITLE Unpublished  
JOURNAL Unpublished  
COMMENT Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
660 South Euclid Avenue  
St. Louis, MO 63110  
Insert Length: 182000 Std Error: 0.00  
Seq primer: BMT TCGACATCACTATGACGAGGA  
Class: BAC ends  
Size: 182000  
High quality sequence start: 35  
High quality sequence end: 681.

FEATURES  
SOURCE 1..940  
Location/Qualifiers  
/organism="Gallus gallus"  
/db\_xref="taxon:633041"  
/db\_xref="taxon:4577"  
/clone\_id="Male Mapping Project/DuPont Consensus  
Library: This sequence is part of a project of EST assembly resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration with the Male Mapping Project.  
Bases 131 g 172 c 25 others

BASE COUNT 304 a 129 c 129 g 129 c 2 others

ORGANISM

Query Match 71.3% Score 21.4; DB 29; Length 940;  
Best Local Similarity 95.7% Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATGTAAGCCGAGAAATGCACTGAC 27  
DB 57 ATGTAAGCCGAGAAATGCACTGAC 35

RESULT 9  
LOCUS A0383884  
DEFINITION A0383884.1 GI:4354907  
ACCESSION A0383884.1 GI:4354907  
KEYWORDS A0383884.1 GI:4354907  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Bakayocet; Neognathae; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1. 654 bp DNA linear GSS 21-MAY-1999  
Seq primer: BMT TCGACATCACTATGACGAGGA  
Class: BAC ends  
Size: 182000  
High quality sequence start: 35  
High quality sequence end: 681.

REFERENCE  
AUTHORS Rasmussen, J., Adams, M.D., Newman, W., Malek, J., de Jong, P., and Venter, J.C.

COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Biotechnology Genomics  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: shaying.zhao@nih.gov  
Clones are derived from the human BAC library RPI-11. For BAC library availability, please contact Piete de Jong ([piete@jcmg.med.buffalo.edu](mailto:piete@jcmg.med.buffalo.edu)). Clones may be purchased from BAC Resource (<http://bacres.med.buffalo.edu/ordering/>) or from [http://www.igb.org/db/hungon/bac\\_and\\_search/bac\\_and\\_search.html](http://www.igb.org/db/hungon/bac_and_search/bac_and_search.html)  
Seq primer: SP6  
Class: BAC ends  
Location/Qualifiers







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On nucleic - nucleic search using sw model  
Run on: December 18, 2003, 09:02:17 / Search time 1343.11 seconds  
(without alignment)  
913.763 Million cell updates/sec

Title: US-09-889-491-13  
Perfect score: 30  
Sequence: 1 atctagagccacgaagaatcagctgacc 30  
Scoring table: IDENTITY UNC  
Gapco 10.0 / Gapext 1.0

Searched: 2886711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing time: 45 summaries

Database :

1: gb\_hai\*  
2: gb\_hag\*  
3: gb\_hag\*  
4: gb\_hag\*  
5: gb\_hag\*  
6: gb\_hag\*  
7: gb\_hag\*  
8: gb\_hag\*  
9: gb\_hag\*  
10: gb\_hag\*  
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12: gb\_hag\*  
13: gb\_hag\*  
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42: gb\_hag\*  
43: gb\_hag\*  
44: gb\_hag\*  
45: gb\_hag\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SWIMMANTS

| Result No. | Score | Query Match Length | ID     | Description |
|------------|-------|--------------------|--------|-------------|
| 1          | 30    | 100.0              | 30 6   | AX028510    |
| 2          | 23.8  | 79.3               | 24.15  | HOMINSP01   |
| 3          | 23.8  | 79.3               | 24.15  | AC104652    |
| 4          | 23.8  | 79.3               | 24.15  | AC104652    |
| 5          | 23.8  | 79.3               | 24.15  | AC104652    |
| 6          | 23.2  | 77.3               | 86.91  | AC004810    |
| 7          | 23.2  | 77.3               | 86.91  | AC102085    |
| 8          | 23.2  | 77.3               | 86.91  | AC102085    |
| 9          | 23.2  | 74.0               | 139.97 | AC010612    |
| 10         | 23.2  | 74.0               | 139.97 | AC134862    |
| 11         | 23.2  | 74.0               | 139.97 | AC009514    |
| 12         | 23.2  | 74.0               | 139.97 | AC009514    |
| 13         | 23.2  | 74.0               | 139.97 | AC010612    |
| 14         | 23.2  | 74.0               | 139.97 | AC010612    |
| 15         | 23.2  | 74.0               | 139.97 | AC010612    |
| 16         | 23.2  | 74.0               | 139.97 | AC010612    |
| 17         | 23.2  | 74.0               | 139.97 | AC010612    |
| 18         | 23.2  | 74.0               | 139.97 | AC010612    |
| 19         | 23.2  | 74.0               | 139.97 | AC010612    |
| 20         | 23.2  | 74.0               | 139.97 | AC010612    |
| 21         | 23.2  | 74.0               | 139.97 | AC010612    |
| 22         | 23.2  | 74.0               | 139.97 | AC010612    |
| 23         | 23.2  | 74.0               | 139.97 | AC010612    |
| 24         | 23.2  | 74.0               | 139.97 | AC010612    |
| 25         | 23.2  | 74.0               | 139.97 | AC010612    |
| 26         | 23.2  | 74.0               | 139.97 | AC010612    |
| 27         | 23.2  | 74.0               | 139.97 | AC010612    |
| 28         | 23.2  | 74.0               | 139.97 | AC010612    |
| 29         | 23.2  | 74.0               | 139.97 | AC010612    |
| 30         | 23.2  | 74.0               | 139.97 | AC010612    |
| 31         | 23.2  | 74.0               | 139.97 | AC010612    |
| 32         | 23.2  | 74.0               | 139.97 | AC010612    |
| 33         | 23.2  | 74.0               | 139.97 | AC010612    |
| 34         | 23.2  | 74.0               | 139.97 | AC010612    |
| 35         | 23.2  | 74.0               | 139.97 | AC010612    |
| 36         | 23.2  | 74.0               | 139.97 | AC010612    |
| 37         | 23.2  | 74.0               | 139.97 | AC010612    |
| 38         | 23.2  | 74.0               | 139.97 | AC010612    |
| 39         | 23.2  | 74.0               | 139.97 | AC010612    |
| 40         | 23.2  | 74.0               | 139.97 | AC010612    |
| 41         | 23.2  | 74.0               | 139.97 | AC010612    |
| 42         | 23.2  | 74.0               | 139.97 | AC010612    |
| 43         | 23.2  | 74.0               | 139.97 | AC010612    |
| 44         | 23.2  | 74.0               | 139.97 | AC010612    |
| 45         | 23.2  | 74.0               | 139.97 | AC010612    |

## ALIGNMENTS

| Result No. | Score | Query Match Length | ID     | Description |
|------------|-------|--------------------|--------|-------------|
| 1          | 30    | 100.0              | 30 6   | AX028510    |
| 2          | 23.8  | 79.3               | 24.15  | HOMINSP01   |
| 3          | 23.8  | 79.3               | 24.15  | AC104652    |
| 4          | 23.8  | 79.3               | 24.15  | AC104652    |
| 5          | 23.8  | 79.3               | 24.15  | AC104652    |
| 6          | 23.2  | 77.3               | 86.91  | AC004810    |
| 7          | 23.2  | 77.3               | 86.91  | AC102085    |
| 8          | 23.2  | 77.3               | 86.91  | AC102085    |
| 9          | 23.2  | 74.0               | 139.97 | AC010612    |
| 10         | 23.2  | 74.0               | 139.97 | AC134862    |
| 11         | 23.2  | 74.0               | 139.97 | AC009514    |
| 12         | 23.2  | 74.0               | 139.97 | AC009514    |
| 13         | 23.2  | 74.0               | 139.97 | AC010612    |
| 14         | 23.2  | 74.0               | 139.97 | AC010612    |
| 15         | 23.2  | 74.0               | 139.97 | AC010612    |
| 16         | 23.2  | 74.0               | 139.97 | AC010612    |
| 17         | 23.2  | 74.0               | 139.97 | AC010612    |
| 18         | 23.2  | 74.0               | 139.97 | AC010612    |
| 19         | 23.2  | 74.0               | 139.97 | AC010612    |
| 20         | 23.2  | 74.0               | 139.97 | AC010612    |
| 21         | 23.2  | 74.0               | 139.97 | AC010612    |
| 22         | 23.2  | 74.0               | 139.97 | AC010612    |
| 23         | 23.2  | 74.0               | 139.97 | AC010612    |
| 24         | 23.2  | 74.0               | 139.97 | AC010612    |
| 25         | 23.2  | 74.0               | 139.97 | AC010612    |
| 26         | 23.2  | 74.0               | 139.97 | AC010612    |
| 27         | 23.2  | 74.0               | 139.97 | AC010612    |
| 28         | 23.2  | 74.0               | 139.97 | AC010612    |
| 29         | 23.2  | 74.0               | 139.97 | AC010612    |
| 30         | 23.2  | 74.0               | 139.97 | AC010612    |
| 31         | 23.2  | 74.0               | 139.97 | AC010612    |
| 32         | 23.2  | 74.0               | 139.97 | AC010612    |
| 33         | 23.2  | 74.0               | 139.97 | AC010612    |
| 34         | 23.2  | 74.0               | 139.97 | AC010612    |
| 35         | 23.2  | 74.0               | 139.97 | AC010612    |
| 36         | 23.2  | 74.0               | 139.97 | AC010612    |
| 37         | 23.2  | 74.0               | 139.97 | AC010612    |
| 38         | 23.2  | 74.0               | 139.97 | AC010612    |
| 39         | 23.2  | 74.0               | 139.97 | AC010612    |
| 40         | 23.2  | 74.0               | 139.97 | AC010612    |
| 41         | 23.2  | 74.0               | 139.97 | AC010612    |
| 42         | 23.2  | 74.0               | 139.97 | AC010612    |
| 43         | 23.2  | 74.0               | 139.97 | AC010612    |
| 44         | 23.2  | 74.0               | 139.97 | AC010612    |
| 45         | 23.2  | 74.0               | 139.97 | AC010612    |









assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are generated and oriented, and separated into scaffolds. The scaffolds are then ordered and oriented, possibly by extending beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc@bcm.tmc.edu

Project information

Center project name: 6677304X12

Summary Statistics

Assembly program: Phrap; version 0.99029  
Consensus quality: 24130 bases at least Q40  
Consensus quality: 24764 bases at least Q20  
Estimated insert size: 262891; sum-of-contigs estimation  
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

Note: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
NOTE: This sequence may represent more than one clone.  
NOTE: This is a 'working draft' sequence. It currently is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequences, and the contigs will be available with the accession number 0111 be preserved.

1 104470: contig of 104470 bp in length  
2 104471 256470: gap of 151940 bp  
3 104472 256471: gap of 151940 bp  
4 104473 256472: gap of 151940 bp  
5 256473 256474: contig of 1117 bp in length  
6 256475 256476: gap of 1117 bp in length  
7 256477 256478: gap of 1117 bp in length  
8 256479 256480: gap of 1117 bp in length  
9 256481 256482: gap of 1117 bp in length  
10 256483 256484: gap of 1117 bp in length  
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13 256489 256490: gap of 1117 bp in length  
14 256491 256492: gap of 1117 bp in length  
15 256493 256494: gap of 1117 bp in length  
16 256495 256496: gap of 1117 bp in length  
17 256497 256498: gap of 1117 bp in length  
18 256499 256500: gap of 1117 bp in length  
19 256501 256502: gap of 1117 bp in length  
20 256503 256504: gap of 1117 bp in length  
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22 256507 256508: gap of 1117 bp in length  
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ACCESSION ACT2008.4 GI:3298228  
VERSION ACT2008.4  
KEYWORDS HTG; HTGS PHASE1; HTGS ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)

CHROMOSOMES Chromosome 10 (Chr10)

Map: 10 (19526) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

REFERENCE  
AUTHORS

Murry D, Marie K, Lee A, Thomson S, Adams C, Alder J, Allen C, Allen H, Albrecht S, Amin A, Anagnostou A, Anagnostou V, Ayoubi A, Ayoubi M, Beale E, Beale H, Belding D, Belding M, Belding N, Belding P, Belding R, Belding S, Belding T, Belding U, Belding V, Belding W, Belding X, Belding Y, Belding Z, Belding AA, Belding AB, Belding AC, Belding AD, Belding AE, Belding AF, Belding AG, Belding AH, Belding AI, Belding AJ, Belding AK, Belding AL, Belding AM, Belding AN, Belding AO, Belding AP, Belding AQ, Belding AR, Belding AS, Belding AT, Belding AU, Belding AV, Belding AW, Belding AX, Belding AY, Belding AZ, Belding BA, Belding BB, Belding BC, Belding BD, Belding BE, Belding BF, Belding BG, Belding BH, Belding BI, Belding BJ, Belding BK, Belding BL, Belding BM, Belding BN, Belding BO, Belding BP, Belding BQ, Belding BR, Belding BS, Belding BT, Belding BU, Belding BV, Belding BW, Belding BX, Belding BY, Belding BZ, Belding CA, Belding CB, Belding CC, Belding CD, Belding CE, Belding CF, 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# COMMENT

On Oct 12, 2002 this sequence version replaced gi:2147300.  
The sequence in this assembly is a combination of BAC based reads  
(http://www.bac.com.tmc.edu/projects/rat/) and contig data  
(http://www.bac.com.tmc.edu/projects/rat/). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly. A 'contig-scaffold'. Within each contig-scaffold  
by sized gaps filled with Ns to the estimated size of the  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
sequence only contigs will be indicated in the feature  
table.

Center: Baylor College of Medicine

Web site: http://www.bac.com.tmc.edu/  
Contact: hspc-helphom.tmc.edu

Project Information

Center project name: OMN1908

Assembly program: Phrap version 0.93029

Consensus quality: 17059 bases at least Q40

Consensus quality: 10645 bases at least Q20

Estimated insert size: 1770421 sum-of-contigs estimation

Quality coverage: 6x in Q40 bases, sum-of-contigs estimation

\* NOTE: Scaffolded insert size may differ from sequence length  
(see http://www.bac.com.tmc.edu/docs/genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently  
consists of 5 contigs. The true order of the pieces  
is arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence  
if it is available and the accession number will  
be preserved.

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184680 188194: contig of unknown length

188195 191782: contig of 3588 bp in length

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191883 193300: contig of 3318 bp in length

193301 193301: contig of 1996 bp in length

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complement(167606..168622)

clone end:SP6

end sequence: RHBSP041V

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clone end:SP6 extension

179471..180554

/note="wgs and extension"

clone\_end:SP6

JOURNAL

TITLE

REFERENCE

AUTHORS

TITLE

Submitted (12-OCT-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

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## TITLE

Stravens, N., Subramanian, A., Tallamraju, S., Reddy, S., Reddy, S.,  
Wajsbort, B., Wu, X., Wymann, D., Vassiliev, H., Vial, R., Vo, A.,  
Zemek, L., Zimmer, A., and Zody, M., Young, G., Zaitoun, J.,  
Submitted (01-SEP-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

## REFERENCE

3 (bases 1 to 169060)

## AUTHORS

Stravens, N., Subramanian, A., Tallamraju, S., Reddy, S., Reddy, S.,  
Wajsbort, B., Wu, X., Wymann, D., Vassiliev, H., Vial, R., Vo, A.,  
Zemek, L., Zimmer, A., and Zody, M., Young, G., Zaitoun, J.,  
Submitted (01-SEP-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

## TITLE

Submitted (08-NOV-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

## REFERENCE

1 (bases 1 to 169060)

## AUTHORS

Stravens, N., Subramanian, A., Tallamraju, S., Reddy, S., Reddy, S.,  
Wajsbort, B., Wu, X., Wymann, D., Vassiliev, H., Vial, R., Vo, A.,  
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Research, 320 Charles Street, Cambridge, MA 02141, USA

## TITLE

Submitted (19-DEC-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

## COMMENT

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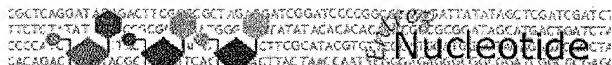
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□1: AX028511. Sequence 14 from ...[gi:10189694]

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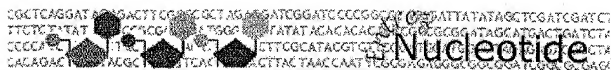
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VERSION     AX028511.1   GI:10189694
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kusk,P.
  TITLE     Genetic predisposition
  JOURNAL   Patent: WO 0042216-A 14 20-JUL-2000;
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NCBI | NLM | NIH

Dec 11 2003 13:29:08



□1: AX028510. Sequence 13 from ...[gi:10189693]

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LOCUS       AX028510                30 bp      DNA            linear      PAT16-SEP-2000
DEFINITION  Sequence 13 from Patent WO0042216.
ACCESSION   AX028510
VERSION     AX028510.1   GI:10189693
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1
  AUTHORS   Kusk,P.
  TITLE     Genetic predisposition
  JOURNAL   Patent: WO 0042216-A 13 20-JUL-2000;
            OSTEOMETER BIOTECH AS (DK) ; KUSK PHILIP (DK)
FEATURES             Location/Qualifiers
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